133 finds: 1   Q09138 77 finds: 1   P80643 253 finds: 1   P80643 253 finds: 1   P90369 357 finds: 1   P9359 187 finds: 1   P33772 376 finds: 1   P33773 360 finds: 1   Q00831 360 finds: 1   Q00831 360 finds: 1   Q01554 360 finds: 1   Q91555 334 finds: 1   Q91555 334 finds: 1   P92694 68 finds: 1   P930894 275 finds: 1   P930894 423 finds: 1   P930894 423 finds: 1   P930894 4240 finds: 1   P930894 427 finds: 1   P930896 448 finds: 1   P930957 213 finds: 1   P54657 294 finds: 1   P54657 294 finds: 1   P49070 136 finds: 1   P49070 137 finds: 1   P49070 138 finds: 1   P49070 139 finds: 1   P49070 130 finds: 1   P49070 131 finds: 1   P49070 132 finds: 1   P49070 133 finds: 1   P49070 134 finds: 1   P49070 135 finds: 1   P49070 136 finds: 1   P49070 137 finds: 1   P49070 138 finds: 1   P49070 139 finds: 1   P49070 130 finds: 1   P49070 131 finds: 1   P49070 132 finds: 1   P49070 133 finds: 1   P49070 134 finds: 1   P49070 135 finds: 1   P49070 136 finds: 1   P49070 137 finds: 1   P49070 138 finds: 1   P49070	SW:CG21_SCHPO ck: 7358 len: SW:CH19_DROGR ck: 4664 len:	ck:	SW:CDSA_HAEIN ck: 8973 len:	SW:CDD_MYCPI ck: 6718 len:	SW:CDD_BACSU ck: 9048 len:	SW:CAMG_MOUSE ck: 283 len:	W:CAD1_DICDI ck: 3813 len:	ck: 3813	ck: 3813	ck: 8425	8425	SW:BRA2_BRAFL ck: 391 len:	SW:BRA1_BRAFL ck: 7365 len:	SW:BR3A_HUMAN ck: 2610 len:	SW:BPHB_PSEPS ck: 1527 len:	SW:BMPB_XENLA ck: 1620 len:	SW:BMPA_XENLA ck: 9714 len:	SW:ATPZ_BACP3 ck: 4392 len:	SW:ATPD_HUMAN ck: 1686 len:	SW:ATP8_PONPY ck: 3550 len:	SW:ATP8_PONPP ck: 3460 len:	SW:ATP8_PONPA ck: 3336 len:	SW:ATP8_PODAN ck: 8763 len:	SW:AT93_HUMAN ck: 2178 len:	SW:ARGC_ECOLI ck: 6342 len:	SW:ARG3_XENLA ck: 4724 len:	SW:ARG2_XENLA ck: 4641 len:	SW:ARG1_XENLA ck: 4321 len:	SW:ANX2_XENLA ck: 6452 len:	SW:AMPD_CITER ck: 4831 len:	SW:AMPC_SERMA ck: 107 len:	SW:AMIA_SALTY ck: 5663 len:	SW:ALR_TREPA ck: 255 len:	SW:ADH2_DROMO ck: 8528 len:	SW:ACP_BACSU ck: 8148 len:	SW:AAKG_PIG ck: 8859 len:
finds: 1   P09369 dr finds: 1   P0933772 sa finds: 1   P09539 se finds: 1   P09539 se finds: 1   P09553 xe finds: 1   P091553 xe finds: 1   P091555 xe finds: 1   P091555 xe finds: 1   P091555 xe finds: 1   P091554 xe finds: 1   P091555 xe finds: 1   P092694 po finds: 1   P092694 po finds: 1   P092694 po finds: 1   P09354 ba finds: 1   P09356 ba finds: 1   P09365 dr finds: 1   P09365 dr finds: 1   P09365 dr finds: 1   P09365 ba finds: 1   P09365 ba finds: 1   P09379 ba finds: 1   P19079 ba finds: 1   P19079 ba finds: 1   P49070 mu finds: 1   P49070 mu	ь ь																						50		334							289				
1 Q09138 st 1 Q09138 st 1 P80643 bz 1 P80643 bz 1 P80643 bz 1 P806346 tz 1 P933772 sa 1 P18539 sc 1 Q00831 cz 1 Q00831 cz 1 Q00831 cz 1 Q00831 cz 1 P24801 xc 1 Q01555 xc 1 P11446 es 1 Q01555 xc 1 P48201 ho 1 P92694 po 1 P92694 po 1 P92896 po 1 P92896 po 1 P93354 ba 1 P08694 ps 1 P08694 ps 1 P08694 ps 1 P08694 ps 1 P08694 ps 1 P08694 ps 1 P300884 xc 1 P33967 ba 1 P54657 dia 1 P49070 mu 1 P49070 mu 1 P490718 my 1 P44937 had 1 P44937 had 1 P44937 had	inds:													inds:																					finds: 1	finds: 1
93643 bz 99369 di 16346 tz 16346 tz 16346 tz 16353 se 16853 se 16853 se 16864 ps 17564 ps 17573 xe 17564 ps 17574 ps 17574 ps 17574 ps 17576 ps 17577 ps 17576 ps 17577 ps 17576 ps 175776 ps 17576 ps 17576 ps 17576 ps 17576 ps 17576 ps 17576 ps 175776 ps 17576 ps 17576 ps 17576 ps 17576 ps 17576 ps 17576 ps 175776 ps 17576 ps	! P2	1 01	! P4.	! P4	. F4	! P4	. P5	. P5	. P5	. P3	. P3	! P8	1 01	1 00	! P0	! P3	! P2	. PO	P3	i Q3	. P9	1 19	: 20	! P4	1 d i	1 Q9	1 29	. 09	- P	. <u>.</u>	. P1	P	Q.	; P(	. P.	
	4865 schizosacc 3427 drosophila	9084 sus	4937 haemophilus	7718 mycoplasma	9079 bacillus	9070 mus	4657 dictyostelium					0492 branchiostoma	7134 branchios	1851 homo	8694 pseudomonas	0884 xenopus	15703 xenopus	9354 bacillus	0049 homo	15584 pongo	12896 pongo	12694 pongo	)2653 podos	18201 homo	11446 escherichia	1555 xenopus	91554 xenopus	91553 xenopus	24801 xenopus	00831 citrobacter	18539 serratia	33772 salmonell		09369 drosophila	80643 bacillus	09138 sus

rattus norvegicus (r	Q64623		finds: 1	len: 367	ck: 6443	SW: DUS1_RAT
mus musculus (mouse)	P28563		finds: 1	len: 367	ck: 5871	SW:DUS1_MOUSE
homo sapiens (human)	P28562		finds: 1	len: 367	ck: 5401	SW:DUS1_HUMAN
vibrio alginolyticus	Q56578		finds: 1	len: 165	ck: 2736	SW:DSBB_VIBAL
bacillus subtilis. d	P39577		finds: 1	len: 252	ck: 2631	SW:DLTE_BACSU
streptomyces cinnamo	P41177		finds: 1	len: 261	ck: 4473	SW:DHKR_STRCM
streptomyces violace	P16542		finds: 1	len: 272	ck: 3104	SW:DHK1_STRVN
rattus norvegicus (r	P47727		finds: 1	len: 276	ck: 3202	SW:DHCA_RAT
oryctolagus cuniculu	P47844		finds: 1	len: 276	ck: 1426	SW:DHCA_RABIT
mus musculus (mouse)	P48758		finds: 1	len: 276	ck: 204	SW:DHCA_MOUSE
homo sapiens carbony	P16152		finds: 1	len: 276	ck: 3202	SW:DHCA_HUMAN
homo sapiens (human)	075828		finds: 1	len: 276	ck: 391	SW:DHC3_HUMAN
anas platyrhynchos (	057314		finds: 1	len: 312	ck: 9157	SW:DHBX_ANAPL
mus musculus (mouse)	070503	_	finds: 1	len: 312	ck: 4788	SW:DHBK_MOUSE
rattus norvegicus (r	054939		finds: 1	len: 306	ck: 3366	SW:DHB3_RAT
mus musculus (mouse)	P70385	-	finds: 1	len: 305	ck: 9317	SW:DHB3_MOUSE
homo sapiens (human)	P37058	_	finds: 1	len: 310	ck: 3434	SW:DHB3_HUMAN
klebsiella pneumonia	Q59477		finds: 1	len: 387	ck: 846	SW:DHAT_KLEPN
citrobacter freundii	P45513		finds: 1	len: 387	ck: 101	SW:DHAT_CITER
streptococcus mutans	Q54433		finds:	len: 145	ck: 9135	SW:DFP_STRMU
saccharomyces cerevi	P20449	-	finds: 1	len: 482	ck: 2958	SW:DBP5_YEAST
streptomyces sp. (st	P39042	1	finds:	len: 291	ck: 4817	SW:DACX_STRSK
escherichia coli. cy	P27111		finds:	len: 299	ck: 4304	SW:CYNR_ECOLI
rhodocyclus tenuis (	860004	,,	finds:	len: 92	ck: 2620	SW:CY2_RHOTE
blaberus craniifer.	P80675	-	finds:	len: 127	ck: 1926	SW:CU04_BLACR
bacillus subtilis. c	P12946	1 ::	finds:	len: 306	ck: 1522	SW:CTAA_BACSU
bacillus firmus. cyt	Q04443	1 :	finds:	len: 297	ck: 716	SW:CTAA_BACFI
escherichia coli. su	P40715	1	finds:	len: 331	ck: 8969	SW:CSCR_ECOLI
pisum sativum (garde	P21727	 L	finds:	len: 402	ck: 5889	SW:CPTR_PEA
cancer pagurus (rock	P81580	1	finds:	len: 114	ck: 1605	SW:CPC1_CANPG
schizosaccharomyces	P79010	1 .	finds:	len: 164	ck: 7810	SW:COX4_SCHPO
schizophyllum commun	P14058	1	finds:	len: 268	ck: 7659	SW:COX3_SCHCO
escherichia coli, ni	P36562	1	finds:	len: 359	ck: 7029	SW:COBT_ECOLI
tobacco streak virus	P03598	<u> </u>	finds:	len: 237	ck: 3595	SW:COAT_TOBSV
turnip crinkle virus	P06663	<u> </u>	finds:	len: 351	ck: 1818	SW:COAT_TCV
rhodobacter sphaeroi	P40685		finds:	len: 213	ck: 8138	SW:CHRR_RHOSH

22034 eacher Tonia	١	THUS	. 6	101.	Ċ	5	om.misq_bcour
oschorichi:		f	) ( ) (		7651	2 (	
ealmonella tu		÷	n n o	<u>.</u>	ν ν		CW.HICS CALLA
! P04233 homo sapiens (human). h	μ	finds:	296	len:	9949	ck:	SW:HG2A_HUMAN
! P50200 clostridium sordellii.	<u>-</u>	finds:	267	len:	1047	œ :	SW: HDHA_CLOSO
! P04187 mus musculus (mouse). g	H	finds:	247	len:	92	ck:	SW:GRAB_MOUSE
! P35411 rattus norvegicus (rat)	μ	finds:	354	len:	4478	c)	SW:GPRD_RAT
! P49238 homo sapiens (human). p	μ	finds	355	len:	2863	ck:	SW:GPRD_HUMAN
! P37606 escherichia coli. glyce	μ	finds:	339	len:	4443	ck:	SW:GPDA_ECOLI
! Q28914 pan troglodytes (chimpa	ב	finds:	123	len:	149	ck:	SW:GLPB_PANTR
! Ol8830 ovis aries (sheep). gro	μ	finds:	375	len:	1548	ck:	SW:GDF8_SHEEP
! 035312 rattus norvegicus (rat)	<u></u>	finds:	376	len:	1496	ck:	SW:GDF8_RAT
! O18831 sus scrofa (pig). growt	μ	finds:	375	len:	1805	ck:	SW:GDF8_PIG
! O18828 papio hamadryas (hamadr	μ	finds:	375	len:	1463	ck:	SW:GDF8_PAPHA
i 008689 mus musculus (mouse). g	<u>, , , , , , , , , , , , , , , , , , , </u>	finds:	376	len:	2293	ck:	SW:GDF8_MOUSE
! O14793 homo sapiens (human). g	μ	finds:	375	len:	1814	ck:	SW:GDF8_HUMAN
! O18836 bos taurus (bovine). gr	 µ	finds:	375	len:	9403	ck:	SW:GDF8_BOVIN
! P41347 zea mays (maize). ferre	 L	finds:	152	len:	4642	ck:	SW:FTRC_MAIZE
! P01100 homo sapiens (human). p	 L	finds:	380	len:	4677	ck:	SW: FOS_HUMAN
! P11939 gallus gallus (chicken)	μ	finds:	367	len:	7007	ck:	SW:FOS_CHICK
! P23050 avian retrovirus nk24.	μ	finds:	322	len:	9324	ck:	SW: FOS_AVINK
! P23449 bacillus subtilis. prob	<u>-</u>	finds:	208	len:	1150	ck:	SW:FLIH_BACSU
1 p37925 salmonella typhimurium.	<u>-</u>	finds:	335	len:	6074	ck:	SW:FIMH_SALTY
! P28891 agkistrodon contortrix	μ	finds:	203	len:	7566	ck:	SW:FIBR_AGKCO
! P28901 shigella flexneri. ferr	μ	finds	135	len:	1251	ck:	SW: FENR_SHIFL
! P28861 escherichia coli. ferre	μ	finds:	247	len:	3071	ck:	SW:FENR_ECOLI
! P55336 vibrio harveyi. 3-oxoac	<u>-</u>	finds:	244	len:	5984	ck:	SW:FABG_VIBHA
! O54438 pseudomonas aeruginosa.	 L	finds:	247	len:	9922	ck:	SW:FABG_PSEAE
! P43713 haemophilus influenzae.	<u> </u>	finds:	242	len:	4159	ck:	SW:FABG_HAEIN
! P25716 escherichia coli. 3-oxc	<u>-</u>	finds:	244	len:	3492	ck:	SW:FABG_ECOLI
! P95376 neisseria meningitidis.	<u>,,</u>	finds	144	len:	5831	ck:	SW:EXBD_NEIME
! 006434 neisseria gonorrhoeae.	μ.	finds:	144	len:	4894	ck:	SW:EXBD_NEIGO
: 033096 mycobacterium leprae. e	 H	finds	318	len:	3764	ck:	SW:ETFA_MYCLE
! Q90257 brachydanio rerio (zebr	 H	finds:	270	len:	1627	ck:	SW:ES1_BRARE
! P39704 saccharomyces cerevisia	 H	finds	215	len:	5386	ck:	SW:ERP2_YEAST
! Q29143 trichosurus vulpecula (	 -	finds	102	len:	5524	ck:	SW:ELAC_TRIVU
! P08761 drosophila melanogaster	 H	finds	255	len:	68	ck:	SW:EI28_DROME
! P35621 brachydanio rerio (zebr		finds:	355	len:	2951	<u>с</u> ::	SW:DVR1_BRARE

SW: NUZM_NEUCR	SW: NUOJ_ECOLI	SW: NUKM_BRAOL	SW: NUHM_NEUCR	SW:NU6M_APILI	SW: NU5M_ANSCE	SW: NU1M_COTJA	SW: NOR1_ASPPA	SW:NIFY_KLEPN	SW: NEUB_XENLA	SW:MTDA_METEX	SM: MML6_MYCTU	SW:MLPA_MYXXA	SW:MESJ_HAEIN	SW:MDH_RHILV	SW:MAUF_PARDE	SW:LSPA_MYCTU	SW:KR1_HSVBS	SW: KDUD_BACSU	SW: ISIA_SYNY3	SW: IS12_STRAL	SW:IPRA_SAGSA	SW: IMPB_SALTY	SW: IMMN_ECOLI	SW:IDNR_ECOLI	SW:IDI_MYCTU	SW:ICW3_PSOTE	SW:ICE2_RAT	SW:IAA5_WHEAT	SW:IAA2_WHEAT	SW:IAA1_WHEAT	SW:HYCD_ECOLI	SW:HUPK_RHILV	SW:HPRK_BACSU	SW:HMPH_MOUSE	SW:HMPH_HUMAN
ck: 7	ck: 2	ck: 9	ck: 3	ck: 6	ck: 1	ck: 6	ck: 7	ck:	ck: 1	ck: 9	ck: 4	ck: 8	ck: 1	ck: ]	ck: 7	ck: 2	ck:	ck:	ck: 4	ck: 4	ck: 1	ck: 6	ck: 6	ck: 2	ck: S	ck: 7	ck: 8	ck: 4	ck: 4	ck:	ck: 6	ck: J	ck: 4	ck: 8	ck: 3
7750	2909	9647	3961	6545	1655	6471	7169	8799	1414	9524	4418	6088	1410	1419	7474	2319	5295	3484	4153	4079	1378	6434	6528	2843	9024	7697	8827	4073	4825	3320	675	1548	4393	8616	3785
len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:	len:						
201	184	215	263	167	214	72	271	229	120	288	397	236	430	320	277	202	467	254	342	256	181	424	131	332	203	207	312	124	123	124	307	370	309	271	270
finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1						
1 P19968 neurospora crassa. n	! P33605 escherichia coli. na	! P42027 brassica oleracea (c	! P40915 neurospora crassa. n	! P34857 apis mellifera ligus	! Q31651 anser caerulescens (	! P24968 coturnix coturnix ja.	! Q00278 aspergillus parasiti	! P09135 klebsiella pneumonia	! P43443 xenopus laevis (afri	! P55818 methylobacterium ext	! Q10773 mycobacterium tuberc	! P38371 myxococcus xanthus.	! P44689 haemophilus influenz	! 033525 rhizobium leguminosa	! P29897 paracoccus denitrifi	! Q10764 mycobacterium tuberc	! Q08097 bovine herpesvirus t	P50842 bacillus subtilis. 2	! Q55274 synechocystis sp. (s	! P23393 streptomyces albus g	! P31608 sagittaria sagittifo	! P18642 salmonella typhimuri	! P09182 escherichia coli. co	! P39343 escherichia coli. l-	! P72002 mycobacterium tuberc	! P10822 psophocarpus tetrago	! P55215 rattus norvegicus (r	! P01084 triticum aestivum (w	! P01083 triticum aestivum (w	! P01085 triticum aestivum (w	! P16430 escherichia coli. fo	! P28153 rhizobium leguminosa	! 034483 bacillus subtilis. h	! P43120 mus musculus (mouse)	! Q03014 homo sapiens (human)

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SW:SUFI_HAE:	1 ! P08706 lycopersicon esculentum	finds: 1	: 181	len:	:: 5240	SW:RBS1_LYCES ck:	SW: RBS
SW:ST14_SOL	1 ! P10647 solanum tuberosum (pota	finds: 1	: 181	len:	c: 4699	SW:RBSO_SOLTU ck:	SW:RBS
SW:SSRB_HUM	1 ! P25544 chromatium vinosum. rub	finds: 1	: 302	len:	: 4295	SW:RBCR_CHRVI ck:	SW:RBC
SW:SSRB_CAN	1 ! Q27297 drosophila melanogaster	finds: ]	: 336	len:	c: 2533	SW:RA51_DROME ck:	SW:RA5
SW:SSR1_R	1 ! P25983 bacillus subtilis. dihy	finds:	: 256	len:	c: 2658	SW:PYRZ_BACSU ck:	SW:PYR
SW:SSR1_MOU	1 ! P96174 vibrio sp. (strain 2693	finds: :	: 310	len:	ck: 5096	SW:PYRB_VIBS2 c	SW: PYR
SW:SSR1_HUM	1 ! P19910 serratia marcescens. as	finds:	: 305	len:	ck: 4826	SW:PYRB_SERMA C	SW: PYR
SW:SSAU_SAL	1 ! P08420 salmonella typhimurium.	finds:	: 310	len:	ck: 2583	SW:PYRB_SALTY C	SW: PYR
SW:SRP_CHL	1 ! 058451 pyrococcus horikoshii.	finds:	: 308	len:	ck: 9980	SW:PYRB_PYRHO c	SW:PYR
SW:SPIR_SPI	1 ! P77918 pyrococcus abyssi. aspa	finds:	: 308	len:	ck: 9304	SW:PYRB_PYRAB c	SW:PYR
SW:SPAL_SAL	1 ! P71808 mycobacterium tuberculc	finds:	: 319	len:	ck: 1547	SW:PYRB_MYCTU c	SW: PYR
SW:SIXA_HAE	1 ! P00479 escherichia coli. aspar	finds:	: 310	len:	ck: 3945	SW:PYRB_ECOLI c	SW:PYF
SW:SIXA_ECC	1 ! 026272 methanobacterium thermo	finds:	: 248	) len:	ck: 5550	SW:PUR7_METTH c	SW:PUF
SW:SECY_RIC	1 ! P50452 homo sapiens (human). d	finds:	: 374	len:	ck: 4145	SW:PTI8_HUMAN c	SW:PT]
SW:S27A_ECC	1 ! P35237 homo sapiens (human). p	finds:	: 376	len:	ck: 300	SW:PTI6_HUMAN c	SW:PT]
SW:RUVB_THE	1 ! P54530 bacillus subtilis. prob	finds:	: 299	len:	ck: 158	SW:PTB_BACSU c	SW: PJ
SW:RS8_SYN	1 ! P15781 bos taurus (bovine). pu	finds:	: 79	l len:	ck: 7861	SW:PSPB_BOVIN c	SW:PSI
SW:RS3_ACF	1 ! P17872 aspergillus tubingensis	finds:	: 331	len:	ck: 609	SW:PME_ASPTU c	SW:PI
SW:RS13_SCI	1 ! Q12535 aspergillus aculeatus.	finds:	1: 331	7 len:	ck: 2447	SW:PME_ASPAC c	. SW: PI
SW:RR8_MAI	1 ! Q12639 mycosphaerella pinodes	finds:	1: 299	3 len:	ck: 8743	SW:PLYA_MYCPO c	SW:PL
SW:RK21_SP:	1 ! P08567 homo sapiens (human). p	finds:	350	6 len:	ck: 1536	SW:PLEK_HUMAN (	SW:PL
SW:RIPB_LO	1 ! P21697 synechocystis sp. (stra	finds:	1: 126	8 len:	ck: 6628	SW:PLAS_SYNY3	SW:PL
SW:RIPA_LU	1 ! Q40708 oryza sativa (rice	finds:	1: 263	5 len:	ck: 1305	SW:PI7A_ORYSA	SW:PI
SW:RIB7_AR	1 ! P16678 escherichia	finds:	1: 252	len:	ck: 804	SW: PHNK_ECOLI	SW:PH
SW:RHO7_HU	1 ! P14697 alcaligenes eu	finds:	1: 246	9 len:	ck: 2829	SW:PHBB_ALCEU	SW: PH
SW:RHL_MA	1 P28795 saccharomyce	finds: 1	n: 441	len:	ck: 166	SW: PEX3_YEAST	SW: PE
SW:RFBB_NE	1 ! P31078 rhodobacter c	finds:	n: 166	5 len:	ck: 1875	SW:PETP_RHOCA	SW:PE
SW:REP2_YE	1 ! Q15077 homo sapiens	finds:	en: 328	_	ck: 7545	SW:P2Y6_HUMAN	SW:P2
SW:REHY_TO	1 ! Q99489 homo sapiens (human).	finds:	en: 341	_	ck: 7167	SW:OXDD_HUMAN	SW:OX
SW:REG5_DR	1 ! P31228	finds:	n: 341	3 len:	ck: 9943	SW:OXDD_BOVIN	KO: MS
SW:RBS_MU	: 1 ! P31317 schizosaccharomyces pom	finds:	n: 327	0 len:	ck: 9240	SW:OTC_SCHPO	SW:C
SW:RBSK_SC	: 1	finds:	n: 301	8 len:	ck: 7498	SW:OTCA_VIBS2	IO: MS
SW:RBS3_SC	1   P28678 drosophila	finds:	n: 374	l len:	ck: 7241	SW:OPS1_DROPS	SW:OF
SW:RBS2_LY	: 1 ! P06002 drosophila melanogaster	finds:	n: 373	8 len:	ck: 4358	SW:OPS1_DROME	SW:OF
SW:RBS1_SC	1 ! P22269 calliphora	finds:	n: 371	)1 len:	ck: 9791	SW:OPS1_CALVI	SW:OF
SW:RBS1_PE	1 ! P08005 salmonella typhim	finds:	len: 306		ck: 4920	SW:OPPB_SALTY	SW:OF
	: 1 ! P31132 escherichia coli. oligo	finds:	len: 306		ck: 5147	SW:OPPB_ECOLI	SW:OI

ilus influ	P44847		ls: 1	finds	311	len:	4	Ü,	W:SUFI_HAEIN
solanum tuberosum (p	Q41495		ls: 1	finds	214	len:	5285	с <u>к</u> :	W:ST14_SOLTU
homo sapiens (human)	P43308		ls: 1	finds:	183	len:	8093	ck:	W:SSRB_HUMAN
canis familiaris (do	P23438		ls: 1	finds:	183	len:	8392	ck:	W:SSRB_CANFA
rattus norvegicus (r	P28646		1s : 1	finds	391	len:	9240	č,	SW:SSR1_RAT
mus musculus (mouse)	P30873		1s: 1	finds:	391	len:	8110	ck:	W:SSR1_MOUSE
homo sapiens (human)	P30872		1s: 2	finds:	391	len:	8652	č.	W:SSR1_HUMAN
salmonella typhimuri	P96069	_	is: 1	finds:	352	len:	3263	ck:	W:SSAU_SALTY
chlamydia psittaci.	P28164	_	is: 1	finds:	134	len:	9648	ck:	SW:SRP_CHLPS
spiroplasma mellifer	P21625	-	ds: 1	finds:	241	len:	9527	ck:	W:SPIR_SPIME
salmonella typhimuri	P39444	1	inds:	fin	432	len:	7477	ck:	SW:SPAL_SALTY
haemophilus influenz	P44164	1	inds:	fin	164	len:	2974	ck:	SW:SIXA_HAEIN
escherichia coli. ph	P76502	1 :		finds:	161	len:	9360	ck:	SW:SIXA_ECOLI
rickettsia prowazeki	Q9zcs5	1		finds:	433	len:	3620	Ö.	SW:SECY_RICPR
escherichia coli. si	P26428	1	••	finds	217	len:	54	ck:	SW:S27A_ECOLI
thermus aquaticus (s	Q56214	1	••	finds	324	len:	3575	ck:	SW:RUVB_THETH
synechocystis sp. (s	P73307	<u>μ</u>	••	finds	133	len:	8926	ck:	SW:RS8_SYNY3
acholeplasma axanthu	P41117	н		finds:	257	len:	7310	ck:	SW:RS3_ACHAX
schizosaccharomyces	P28189		ds:	finds	150	len:	3858	Ωķ:	SW:RS13_SCHPO
marchantia polymorph	! P06362	ц	finds:		: 132	len:	6002	οk:	SW: RR8_MARPO
spinacia oleracea (s	P24613	1	ds:	finds	: 256	len:	718	ck:	SW:RK21_SPIOL
l luffa cylindrica (sm	P22851	1	finds:		: 250	len:	7681	ck:	SW:RIPB_LUFCY
i luffa cylindrica (sm	900465	₽	finds:		: 277	len	429	čķ:	SW:RIPA_LUFCY
archaeoglobus fulgid	1 028272	1	finds:		: 219	len	4460	ck:	SW:RIB7_ARCFU
3 homo sapiens (human)	P52198	÷	finds:		: 227	len	2901	∘ ck	SW:RHO7_HUMAN
9 macaca mulatta (rhes	228849	ц	ids:	5 finds	: 416	len	: 4371	ck:	SW:RHL_MACMU
l neisse <b>ria gonorrhoea</b>	! P37761	1	ds:	6 finds	: 346	len	: 5086	ck:	SW:RFBB_NEIGO
2 saccharomyces cerevi	P03872	┙	finds:		: 296	len:	: 6596	ck:	SW:REP2_YEAST
4 tortula ruralis (mos	! P52574	ш	finds:		: 218	) len:	: 4850	<u>و</u>	SW:REHY_TORRU
3 drosophila melanogas	94913	Н	finds:		: 298	len:	: 7903	č	SW:REG5_DROME
	! 024045	Н	finds:		: 180	len:	: 2518	ck:	SW:RBS_MUSAC
schizosaccharomyce	1 060116	1	finds:		: 318	len:	: 3214	ck:	SW:RBSK_SCHPO
4 solanum tuberosum (p	! P32764	Н	finds:		: 181	len:	: 4433	ck:	SW:RBS3_SOLTU
9 lycopersicon esculen	! P07179	Ľ	finds:		: 180	5 len:	: 4535	ck:	SW:RBS2_LYCES
4 solanum tuberosum (p	! P26574	1	finds:		: 181	3 len:	: 4863	ck:	SW:RBS1_SOLTU
4 petunia sp. (petunia	! P04714	٢	finds:		: 180	7 len:	: 2967	ck:	SW:RBS1_PETSP

P13461 agrobacterium rhizogend	1 ! P1:	finds:	1: 147	len:	2761	ck:	SW:VID1_AGRRA
P05357 agrobacterium tumefacie	1 ! PO!	finds:	1: 230	len	2826	ck:	SW:VIB8_AGRT9
p09781 agrobacterium tumefacie	1 ! 10	finds:	1: 230	len	2646	ck:	SW:VIB8_AGRT6
P17798 agrobacterium tumefacie	1 ! P1	finds:	1: 237	len:	5994	ck:	SW:VIB8_AGRT5
Q01017 herpesvirus saimiri (st	1 ! 00:	finds:	1: 366	len:	7071	ck:	SW:VGLM_HSVSA
p13291 herpes simplex virus (t	1 ! PI:	finds:	1: 372	len:	501	ck:	SW:VGLI_HSV2H
P03644 bacteriophage g4. major	1 ! PO:	finds:	1: 177	len:	4484	ck:	SW:VGG_BPG4
Q03544 bacteriophage p22. eaa	1 ! 00:	finds:	1: 317	len:	7758	ck:	SW:VEAA_BPP22
P36796 human papillomavirus ty	1 ! P3	finds:	1: 368	len:	4491	ck:	SW:VE2_HPV52
P26547 human papillomavirus ty	1 ! P2	finds:	1: 358	len:	1816	ck:	SW:VE2_HPV51
P36794 human papillomavirus ty	1 ! P3	finds:	1: 368	len:	5828	ck:	SW:VE2_HPV45
P17383 human papillomavirus ty	1 ! P1	finds:	1: 372	len:	9656	ck:	SW:VE2_HPV31
P25482 human papillomavirus ty	1 ! P2	finds:	1: 391	len:	734	ĊĶ:	SW:VE2_HPV2A
P50771 human papillomavirus ty	1 ! P5	finds:	1: 376	len:	1816	ck:	SW:VE2_HPV28
P06790 human papillomavirus ty	1 ! 10	finds:	1: 365	len:	5006	ck:	SW:VE2_HPV18
P36781 human papillomavirus ty	1 ·! P3	finds:	1: 376	len:	273	ck:	SW:VE2_HPV10
P36778 human papillomavirus ty	1 ! P3	finds:	383	len:	4819	ÇK:	SW:VE2_HPV03
Q06240 enterococcus faecium (s	1 ! 00	finds:	1: 384	len:	3601	ck:	SW: VANS_ENTFC
P32517 equine herpesvirus type	1 ! P3:	finds:	1: 303	len:	5996	Ck:	SW:US02_HSVEK
P04153 escherichia coli. umud	1 ! PO	finds:	1: 139	len:	8403	ck:	SW:UMUD_ECOLI
P52487 drosophila melanogaster	1 ! P5:	finds:	1: 153	len:	1891	ck:	SW:UBC7_DROME
P01404 dendroaspis angusticeps	1 ! PO:	finds:	1: 81	len:	8703	ck:	SW:TXF8_DENAN
23441 rattus norvegicus (rat)	1 ! P2	finds:	1: 372	len:	8099	ck:	SW:TTF1_RAT
P50220 mus musculus (mouse). t	1 ! P5	finds:	1: 372	len:	7622	ck:	SW:TTF1_MOUSE
P43699 homo sapiens (human). t	1 ! P4:	finds:	1: 371	len:	5439	ck:	SW:TTF1_HUMAN
P43698 canis familiaris (dog).	1 ! P4:	finds:	1: 371	len:	4988	ck:	SW:TTF1_CANFA
P27710 cryptococcus neoformans	1 ! P2	finds:	1: 312	len:	2342	ck:	SW:TRPF_CRYNE
P50165 datura stramonium (jims	1 ! P5	finds:	1: 268	len:	5293	ck:	SW:TRNH_DATST
Q12093 saccharomyces cerevisia	1 ! Q1:	finds:	1: 417	len:	8415	ck:	SW:TRMU_YEAST
013947 schizosaccharomyces pom	1 1 01	finds:	1: 415	len:	7997	ck:	SW:TRMU_SCHPO
P72828 synechocystis sp. (stra	1 ! P7:	finds:	1: 231	len	6210	ck:	SW:TRMD_SYNY3
Q57471 agrobacterium tumefacie	1 ! Q5	finds:	1: 102	len	4597	ck:	SW:TRAM_AGRT6
070548 mus musculus (mouse). t	1 ! 07	finds:	1: 167	len	5613	ck:	SW:TELT_MOUSE
015273 homo sapiens (human). t	1 1 01:	finds:	1: 167	len:	3375	ck:	SW:TELT_HUMAN
P36402 homo sapiens (human). t	1 ! P3	finds:	1: 269	len:	5007	ck:	SW:TCF1_HUMAN
P52283 chlorella virus il-3a (	1 ! P5:	finds:	: 278	len:	7233	ck:	SW:T2C1_CHVI3
P50235 rattus norvegicus (rat)	1 ! P5	finds:	1: 285	len:	800	č.	SW:SUH3_RAT

20 escherichia coii.	: 23220	-	I Inds:	K	en:	a	cx:	SW: YABP_ECOLL
pseudomonas	! P21485	, р	finds:		len:	6657	. Č	
95 methanococcus	! Q58395	-	. finds:	329	len:	9981	c :	SW:Y988_METJA
57 mycobacterium	! P71557	Н	finds:	282	len:	883	ck:	SW:Y953_MYCTU
33 methanococcus	! P81233	ь	finds:	170	len:	2865	ck:	SW:Y79B_METJA
28 borrelia burgdorferi	1 051728	Ъ	.finds:	440	len:	1619	ck:	SW:Y788_BORBU
11 methanococcus	! P81311	μ	finds:	102	len:	4119	ck:	SW:Y70A_METJA
26 methanococcus	1 057926	H	finds:	406	len:	6767	ck:	SW:Y503_METJA
61 rhizobium sp.	! P55661	٦	finds:	231	len:	6923	ck:	SW:Y4TG_RHISN
34 rhizobium sp.	! P55434	٣	finds:	248	len:	5477	ck:	SW:Y4EK_RHISN
12 mycoplasma pneumonia	! P75112	1	finds:	385	len:	5866	ck:	SW:Y464_MYCPN
02 mycoplasma genitaliu	! P47702	٢	finds:	385	len:	2836	ck:	SW:Y464_MYCGE
72 mycoplasma pneumonia	! P75172	ш	finds:	450	len:	2944	ck:	SW:Y425_MYCPN
88 treponema pallidum.	1 083388	۳	finds:	477	len:	4876	ck:	SW:Y373_TREPA
22 mycoplasma genitaliu	! P47522	ч	finds:	265	len:	9511	čķ:	SW:Y280_MYCGE
85 mycoplasma pneumonia	! P75485	μ	finds:	309	len:	6533	οķ:	SW:Y209_MYCPN
51 mycoplasma genitaliu	! P47451	۲	finds:	308	len:	590	ck:	SW:Y209_MYCGE
53 homo sapiens (human)	1 Q15053	1	finds:	153	len:	4815	ck:	SW:Y040_HUMAN
30 orgyia pseudotsugata	1 010280	1	finds:	298	len:	562	c):	SW:Y021_NPVOP
39 drosophila melanogas	1 P40589	٢	finds:	389	len:	8394	ck:	SW:WNT4_DROME
15 mus musculus (mouse)	! P48615	۲	finds:	354	len:	1689	ck:	SW:WN11_MOUSE
14 homo sapiens (human)	1 096014	1	finds:	354	len:	3073	ck:	SW:WN11_HUMAN
91 coturnix coturnix ja	! P51891	1	finds:	354	len:	4030	ck:	SW:WN11_COTJA
39 gallus gallus (chick	! P49339	1	finds:	354	len:	4630	ck:	SW:WN11_CHICK
41 salmonella typhimuri	! P13041	1	finds:	297	len:	7032	ck:	SW:VRPR_SALTY
17 salmonella dublin.	! P24417	1	finds:	297	len:	7061	œk:	SW:VRPR_SALDU
79 bacteriophage phi-6	! P07579	1	finds:	149	len:	6252	c):	SW:VP8_BPPH6
27 potato virus m	! P17527	٢	finds:	109	len:	3415	cx:	SW:VMEM_PVMR
31 lily virus x. hypoth	1 P27331	۲	finds:	108	len:	8138	ck:	SW:VMEM_LVX
89 chrysanthemum virus	! P37989	۲	finds:	106	len:	566	ck:	SW: VMEM_CVB
32 ovine respiratory	! Q84132	щ	finds:	186	len:	6559	c):	SW:VMA2_ORSVW
45 human respiratory	! P04545	1	finds:	194	len:	9828	ck:	SW:VMA2_HRSVA
92 bovine respiratory	! P29792	μ	finds:	186	len:	6337	ck:	SW:VMA2_BRSVA
30 orgyia pseudotsugata	1 010330	ъ	finds:	374	len:	689	ck:	SW:VLF1_NPVOP
57 agrobacterium	: P06667	۲	finds:	147	len:	4145	ck:	SW:VID1_AGRT6
91 agrobact <b>erium</b>	1 P18591	μ	finds:	147	len:	2312	ck:	SW:VID1_AGRT5

-	p77396 escherichia coli. hypou	finds: 1	len: 285	ck: 4986		SW:YPDC_ECOLI
	•	finds: 1	len: 238	ck: 2171		SW:YOXD_BACSU
	caenorhabditis ereg	finds: 1	len: 161	ck: 9212		SW:YOTC_CAEEL
z! (5	thermoproteus t	finds: 1	len: 232	ck: 9154		SW:YORL_TTV1
vi	caenornabditts erege	finds: 1	len: 381	ck: 431	-	SW:YNU6_CAEEL
<sub>L</sub>	caenornabultis		len: 336	ck: 399	_	SW:YNC9_CAEEL
	caenorhabditis	finds: 1	len: 170	ck: 5825		SW:YNA1_CAEEL
i	saccharomyces c	finds: 1	len: 139	ck: 7226		SW:YNO6_YEAST
X H Z		finds: 1	len: 69	ck: 7679		SW:YM27_MARPO
١		finds: 1	len: 79	8141	ı ck:	SW:YKFF_ECOLI
	es cere	finds: 1	len: 196	8234	i ck:	SW:YJR8_YEAST
	p39430 enterobacter aerogenes	finds: 1	len: 54	4167	E ck:	SW:YJJX_ENTAE
	P39411 escherichia coli. hypot	finds: 1	len: 173	. 3873	ck:	SW:YJJX_ECOLI
_	ım tube	finds: 1	len: 317	1836	σ ck:	SW:YJ96_MYCTU
	1 Q50604 mycobacterium tubercuid	finds: 1	len: 164	7074	U ck:	SW:YI29_MYCTU
	! P46851 escherichia coil Hypor	finds: 1	len: 197	1678	ı ck:	SW:YHGN_ECOLI
,	saccharomyces cere	finds: 1	len: 429	5569	r ck:	SW:YHG3_YEAST
_	bacillus subti	finds: 1	len: 302	1929	J ck:	SW:YHCT_BACSU
	cryphonectria paras	finds: 1	len: 319	3269	ck:	SW:YHA1_CRYPA
		finds: 1	len: 66	9954	ck:	SW:YGLR_STRCO
 H	saccharomyces	finds: 1	len: 107	6897	ck:	SW:YGK9_YEAST
	bacteriophage	finds: 1	len: 148	7782	ck:	SW:YG29_BPSP1
i o	mycobacterium cuberc	finds: 1	len: 148	497	ck:	SW:YF58_MYCTU
		finds: 1	len: 128	5798	ck:	SW:YER4_YEAST
Dat	schizosaccharo	finds: 1	len: 344	3748	ck:	SW:YDTG_SCHPO
//Er	schizosaccharomyces	finds: 1	len: 174	8869 16	ck:	SW:YDSA_SCHPO
	schizosaccharomyces	finds: 1	len: 131	6054 le	ck:	SW:YDM1_SCHPO
	۲	finds: 1	len: 317	1969 le	ck:	SW:YCQ5_YEAST
	escherichia co	inds: 1	len: 299 f	51 le	ck:	SW:YCJZ_ECOLI
	0011.	inds: 1	len: 262 f	6021 le	ck:	SW:YCJI_ECOLI
	escherichia coli.	finds: 1	78	1943 len:	ck:	SW:YCGZ_ECOLI
	0011	finds: 1	182	3224 len:	ck:	SW:YCBQ_ECOLI
	rpurea.	inds: 1	291 f	4681 len:	ck:	SW:YC38_PORPU
	D D	finds: 1	299	2920 len:	с <u>к</u> :	SW:YC21_METJA
	Q48454 klebsiella pneumoniae	finds: 1	373	4280 len:	ck:	
	O31458 bacillus subtilis. hypo	finds: 1	249	3388 len:	ck:	SW:YBFT_BACSU
	ter capsula	finds: 1 !	192	2127 len:	ck:	SW:YBCC_RHOCA

```
End of list
                                                                                                                                                                                                    SW:YPQQ_KLEPN
                                                                                                                                                                                                                         SW:YPJG_BACSU
                                                                                                                                                                                 SW:YQCE_ECOLI
                   SW:ZRP4_MAIZE ck: 6645
                                                                                                  SW:YRKG_BACSU
                                                                                                                     SW:YRBC_HAEIN
                                                                                                                                          SW:YR7B_ECOLI
                                                                                                                                                             SW:YQEK_ECOLI
                                                            SW:YWFF_BACSU
                                                                               SW:YU73_MYCTU
                                        SW:YYVP_CAEEL
                                                                                                                                                              ck: 8893
                                                                                                                                                                                  ck: 1867
                                                                                                                                                                                                        ck: 9681
                                                                                                                                                                                                                            ck: 3316
                                                                                                    ck: 1724
                                                                                                                                             ck: 6140
                                                              ck: 3644
                                                                                 ck: 3649
                                                                                                                          ck: 1216
                                          ck: 1176
                                                                                                                                                                                                                              len: 224
                                                                                                                                                                                                         len: 271
                                                                                                                                             len: 169
                                                                                                                                                                  len: 141
                                                                                                                                                                                    len: 425
                      len: 364
                                                                                                       len: 36
                                                                                                                          len: 214
                                            len: 274
                                                              len: 394
                                                                                    len: 118
                                                                                                                                                                    finds: 1
                                                                                                                                                                                       finds: 1
                                                                                                                                                                                                            finds: 1
                                                                                                                                                                                                                                finds: 1
                                                                                                        finds: 1
                                                                                                                            finds: 1
                                                                                                                                                 finds: 1
                                                                  finds: 1
                                                                                     finds: 1
                           finds: 1
                                             finds: 1
                                                                                                                                                                                        ; P77031 escherichia coli. hy
                                                                                                                                                                                                             ; P27509 klebsiella pneumonia
                                                                                                                                                                                                                                ! P42981 bacillus subtilis. h
                                                                                                                                                                        i P77136
                                                                                                         ! P54434 bacillus subtilis. h
                                                                  ; p39642 bacillus subtilis. h
                                                                                      ! p95085 mycobacterium tuberc
                           1 P47917 zea mays (maize). O-
                                                                                                                            P45028 haemophilus influenz
                                                                                                                                                  P21316 escherichia coli. hy
                                              Q93834 caenorhabditis elega
                                                                                                                                                                      escherichia coli. hy
```

stabases searched: SWISS-PROT, Release 38.1, Released on 20Nov1999, Formatted on 28Dec1999

Total finds: 337
Total length: 29,864,866
otal sequences: 82,229
CPU time: 03:12.78

FINDPATTERNS on Swiss-Prot: \* allowing 0 mismatches

 $1 < (X) \{1,200\} (L,I,V,M,A,P) \\ X (P,T,S) (L,I,V,M,A,P) \\ X (L,I,V,M,A,F,Y,W) (C,T,S) (R,V,M,A,P) \\ X (L,I,V,M,A,F,Y,W) (C,T,S) (R,V,M,A,P) \\ X (L,I,V,M,A,F,Y,W) (L,I,V,M,A,P) \\ X (L,I,V,M,A,P,Y,W) (L,I,V,M,A,P) \\ X (L,I,V,M,A,P,Y,W) (L,I,V,M,A,P) \\ X (L,I,V,M,A,P,Y,W) (L,I,V,M,A,P) \\ X (L,I,V,M,A,P,Y,W) (L,I,V,M,A,P,W) \\ X (L,I,V,M,A,P,Y,W) (L,I,V,M,A,P,W) \\ X (L,I,V,M,A,P,Y,W) (L,I,V,M,A,P,W) \\ X (L,I,V,M,A,P,W) (L,I,V,M,A,P,W) \\ X (L,I,V,M,A,P,W) (L,I,V,M,A,P,W) \\ X (L,I,V,M,A,P,W,W) (L,I,V,M,A,P,W) \\ X (L,I,V,M,A,W,W) (L,I,V,M,A,W,W) \\ X (L,I,V,M,A,W,W,W) \\ X (L,I,V,M,A,W,W) (L,I,V,M,A,W,W) \\ X (L,I,V,M$ 

AAKG\_PIG 1: ck: 8859 len: 133 ! Q09138 sus scrofa (pig). 5'-amp-activate <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,F);(B)(A)x(P)(V)xx(Y)(S)(K)xx(V)xxx(A)x(42)
LVYFDTSLQVKSALVQIYELEEHKXPVIDPESGNTLYILIXKLFITEFPKPEFMSKSLEELQI</pre>

ACP\_BACSU ۲. ck: 8148 len: 77 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,E,X,Y)(L)xx(V)(T)(K)xx(V)xxx(G)x(60)
MADTLERVTKIIVDRLGVDEADVKLEASFKEDLGADSLDVVELVMELEDEFDMEISDEDAE</pre> ; p80643 bacillus subtilis. acyl carrier p

! p09369 drosophila mojavensis (fruit fly)

ALR\_TREPA ck: 255 len: 357 ı Q56346 treponema pallidum. alanine racem

AMIA\_SALTY ck: 5663 len: 289 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W p33772 salmonella typhimurium. probable

```
1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C X{90}(E)X(P)X(P)X(P)X(A)XXX(G)X{254}

MSIRSNEVRLLKKQVNITIKLOKKCSHSVAVIGAPESKGQKRRGVEHGPAAIRSAGLIDRLSNLGCN
PPIPGESWAKPCLSKSDIVYIGLRDLDPAGGFIKNYNISYYSWRHIDDMGIRKVM
EKTFDQLLGRRDRPIHLSFDIDAFDPALAPATGTPVIGGLTYREGVYITEEIHNTGMLSALDLVEVNPVLATTSEEVKATANLAVDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(9)x(D)(L)(X)X(A)XXX(S)X(254)

1: MSIRSNEVELKKÖVSIKLÖKKCSHSVAVIGAPESKGQKRRGVEHGPAAIRSAGLIERLSNLGCN
PPIPGFSWAKPCLSKSDIVYIGLRDLDPAROFILKNYNISYYSWRHIDOMGKIKVM
EKTFDQLLGRRDRPIHLSFDIDAFDPALAPATGTPVIGGLTYREGVYITEEIHNTGMLSAVDLVEVNPVLAATSEEVKATANLAVDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTTSSDKEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x{2,2}(A)x(T);(L)xx(M)(S)(H)xx(A)xxx(T)x(251)

MSTFKLLKTLTSRRQVLKTGLAALTLSGMSHAVAKEETLKTSNGHSKPKTKKTGSKRLVMLDPGHG
ATDRDHLLQQVLFDLVQTDTIKNSLTLGSHIKKKIKPHKLHSRTTEQAAFVVVLKS
PSIPSVLVETSFITNPEEERLLGTTAFRQKIATALANGIISYFHWFDNQKAHTKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARG1_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARG3_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARG2_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANX2_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMPD_CITER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMPC_SERMA
                                                                                                AT93_HUMAN
                                                                                                                                                                                                                                                                                                                 ARGC_ECOLI
                                                                                                                                                                                                                                                                                                                 ck: 6342 len: 334 ! P11446 escherichia coli. n-acetyl-gamma-gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 107
<(x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x[23](P)x(S)(A)xx(L)(S)(R)xx(A)xxx(G)x{103}
MFACAKLACTPSLIRAGSRVAYRPISASVLSRPEASRTGEGSTVFNGAQNGVSQLIQREFQTSAIS</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ck: 4724 len: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ck: 4641 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 4321 len: 360
                                                                                                ck: 2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ck: 6452 len: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <(X)\{1,200\}(L,I,V,M,A,F)X(P,T,S)(L,I,V,M,A,F)XX(L,I,V,M,A,F,Y,M)(X,I,64\}(P)X(P)(A)XX(W)(S)(R)XX(A)XXX(T)X\{7\} \texttt{MLLENGWLVDARHVPSPHHDCRPEDEKPTLLVVHNISLPPGEFGGPWIDALFTGTIDPDAHPFFA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ck: 4831 len: 187
                                                                                                len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  len: 376
                                                                                                142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! Q91555 xenopus laevis (african clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Q91554 xenopus laevis (african clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! P24801 xenopus laevis (african clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Q00831 citrobacter freundii, and enteroba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ! P18539 serratia marcescens. beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ! Q91553 xenopus laevis (african clawed
                                                                                                P48201
                                                                                             homo
                                                                                                sapiens
                                                                                                AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{68}(V)x(T)(L)xx(L)(S)(R)xx(L)xxx(A)x{43}
MGNLQAMFWRQVRYILYLLAIYTLGFGFTPYKTVFLSLILGTSISLLMVWNLTWKIEKFGQ</pre>
```

ATP8 PODAN	ck: 8763 len: 50   002653 podospora anserina, atp synthase
1:	<pre>&lt;(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x[20](A)x(T)(Y)xx(L)(S)(K)xx(L)xxx(V)x{14} MPQLVPYYFVNEITFTFIILAITVYILSKYILPRFVRLFLSRTFISKLLG</pre>
ATP8_PONPA	ck: 3336 len: 68 ! P92694 pongo pygmaeus abelii (sumatran o
:	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{34}(P)x(T)(P)xx(F)(T)(K)xx(L)xxx(P)x{18} MPQLNTTTWPTIITPMLLALFLITQLKLLNSHLHPPTPPKFTKPKLHAKPWGPKWTKVYLP</pre>
ATP8_PONPP	ck: 3460 len: 68 ! P92896 pongo pygmaeus pygmaeus (bornean
1:	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{34}(P)x(T)(P)xx(F)(T)(K)xx(P)xxx(P)xxx(P)XX(18) MPQLNTTWLTIITPTLLALFLITQLKLLNSHLHPPTPPKFTKTKPHAKPWELKWTKIYSP</pre>
ATP8_PONPY	ck: 3550 len: 68 ! Q35584 pongo pygmaeus (orangutan). atp s
<b>1</b> :	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(34}(P)x(T)(P)xx(F)(T)(K)xx(P)xxx(P)xxx(P)X{18} MPQLNTTWLTVITPTLLALFLITQLKLLNSHLHPPTPPKFTKTKPHAKPWELKWTKIYSP</pre>
ATPD_HUMAN	ck: 1686 len: 168 ! P30049 homo sapiens (human). atp synthas
<b>:</b>	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{141}(Y)x(T)(A)xx(A)(T)(R)xx(I)xxx(I)x{11} MLPAALLRRPGLGRLVRHARAYABAAAAPAAASGPNQMSETFASPTQVFFNGANVRQVDVPTL</pre>
ATPZ_BACP3	ck: 4392 len: 127   P09354 bacillus ps3 (thermophilic bacter

HLDNDKNVPKKHVRISRSLTPDKDNWPQIRPLLVTFSHDGKGHALHKRQKRQARHKQRKRLKSSCRRHPLYVDFSDVGWNDWIVA
IVKPAAAASRGPVVRLLDTRLVHHNESKWESFDVTPAIARWIAHKQPNHGFVVEVN
1: MVAGIHSLLLLLFYQVLLSGCTGLIPEEGKRKYTESGRSSPQQSQRVLNQFELRLLSMFGLKR
$x{178}(V)x(P)(A)xx(A)(S)(R)xx(V)xxx(L)x{204}$
BMPA_XENLA CK: 9/14 len: 398   P25/03 xenopus laevis (airican clawed ir

x(178](V)x(P)(A)xx(A)(S)(R)xx(V)xxx(L)x(204)  MVAGIBSLLLLFYQVLLSGCTGLIPEGKRKYTESGRSSFQQSGRVLNQFELRLLSMFGLKR IVKPAAAASRGPVVRLLDTRLYHHUSSKWESFEVYFALARWIJAHKQPHGFVVEVN HLDNDKNVPKKHVRISRSLTPDKDNWPQIRPLLVTFSHDGKGHALHKRQKRQARHKQRKRLKSSCRRHPLYVDFSDVGWNDWIJVA
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	ΕIJ	_	
врнв_рѕерѕ	$ \begin{array}{c} x\{178\}(V)x(P)(A)xx(A)(S)(R)xx(V)\\ wvagihslllqpyqillsgctglvpeegkrkys\\ ivkpaaaasrgpvvrlldtrlihhneskwessdvtpaitkwiahkqpnhgfvvrvt\\ Hldndtnvpkrhvrisrsltldkghwprirpllvtfshdgkghalhkrqkrqarhk\\ \end{array} $		BMPB_XENLA
ck:	HHN HHN X WYA	× ×	ck:
1527	{178}( GIHSLL ESKWES WPRIRP	) {1,20	1620
len:	V)x(P) LLQFY( EDVTP)	0)(L,:	len:
275	)(A)xx DILLSG AITRWI SHDGKG	E, V, M,	398
врнв_PSEPS ck: 1527 len: 275 ! P08694 pseudomonas pseudoalcaligenes. bi	x{170}(V)x(P)(A)xx(A)(S)(R)xx(V)xxx(L)x{204}  MVAGIHSLLLLQFYQILLSGCTGLVPEEGKRKYSESTRSSPQQSQQVLDQFELRLLNMFGLKR IVKPAAAASRGPVVRLLDTRLIHHNESKWESFDYTPAITRWIAHKQPWHGFVVEVT HLDNDTNVPKRHVRISRSLTLDKGHWPRIRPLLVTFSHDGKGHALHKRQKRQARHKQRKRLKSSCRRHPLYVDFSDVGWNDWIVA	<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W	BMPB_XENLA ck: 1620 len: 398 ! P30884 xenopus laevis (african clawed fr
b1	GLKR	×	ĝ fr

$<(X)\{1,200\}(E,I,V,M,A,P)X(P,T,S)(E,I,V,M,A,P)XX(E,I,V,M,A,F,Y,$
$x{123}(A)x(P)(A)xx(A)(S)(R)xx(V)xxx(I)x{136}$
1: MKLKGEAVLITGGASGLGRALVDRFVAEAKVAVLDKSAERLAELETDLGDNVLGIVGDVRSL
3VGPGGMNSDMRGPSSLGMGSKAISTVPLADMLKSVLPIGRMPEVEEYTGAYVFF
FRGDAAPASGALVNYDGGLGVRGFFSGAGGNDLLEOLNIHP

FFVL sus scrofa (plg). corne	len: ] )0}(L,I ()x(T)( )KLNELI	CDD_BACSU ck: 9048 len: 136 ! p19079 bacillus subtilis. cytidine deaminas <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)x(B)(P)xx(A)(C)x(B)(B)xx(C)x(B)(B)xx(C)x(B)(B)(B)xx(C)x(B)(B)xx(C)x(B)(B)xx(C)x(B)xx(C)x(B)(B)xx(C)x(B)xx(C)x(B)xx(C)x(B)xx(C)x(C)x(B)xx(C)x(C)x(C)x(C)x(C)x(C)x(C)x(C)x(C)x(	CAMG_MOUSE ck: 283 len: 294 ! p49070 mus musculus (mouse). calcium-signal  <(X){1,200}{L,I,V,M,A,P}X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)  1	DICDI ck: 3813 len: 213   p54657 dictyostelium discoideum (slime mold <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(G <,X){1,200}(L)X(S)(X)XX(V)XXX(A)X(118) x(P)XX(S)(X)XX(V)XXX(A)X(118) x(P)XX(S)XX(S)XX(S)XX(S)XX(S)XX(S)XX(S)XX		<u> </u>		<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W)(d)</pre>
TKEHNIGLETSILYWHEYDLVWLFLFLVVYFWGGA  TKEHNIGLETSILYWHEYDLVWLFLFLVVYFWGGA  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio  COX4_SCHPO ck: 7810 len: 164 ! p79010 schizosaccharomyces pombe (fissio	DVLAKVGGFDLVGLAGVALLOGRAGUE  COX3_SCHCO ck: 7659 len: 268 ! p14058 schizophyllum commune (bracket fu  COX3_SCHCO ck: 7659 len: 268 ! p14058 schizophyllum commune (bracket fu  COX3_SCHCO ck: 7659 len: 268 ! p14058 schizophyllum  COX3_SCHCO ck: 7	COBT_ECOLI ck: 7029 len: 359 i p36562 escherichia coli nicotinate-nucl  (X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W  (X)[1,200](L,I,V,M,A,P)X(A)XXX(L)X[206]  x[137](1)x(5)(A)xxX(M)(5)(R)xxX(L)X(1)x(206)  x[137](1)x(5)(A)xxX(M)(5)(R)xxX(L)XX(L)X(1)x(206)  x[137](1)x(5)(A)xxX(M)(5)(R)xxX(L)XX(L)XX(L)X(1)x(1)x(1)x(1)x(1)x(1)x(1)x(1)x(1)x(1)x	COAT_TOBSV ck: 3595 len: 237 ! p03598 tobacco streak virus (strain wc)  <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)  1	)XX(L,I,V,M,A,F LSPVAQPVQKVTRLS LENADASDFSVLGEA	(22)(A)X(B)(T)XX(A)(T)(H)XX (22)(A)X(S)(L)XX(A)(T)(H)XX RHHYSDALLTAYAAGTLSBAFSLVVAT LPKLVQPFFRI	1: 1: NYGSQ	CG21_SCHPO ck: 7358 len: 415 i p24865 schizosaccharomyces pomuee  <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,P)X(L,I,V,M,A,P)X(L,I,V,M,A,P)X(L,I,V,M,A,P)X(L,I,V,M,A,P)X(L,I,V,M,A,P)X(L,I,V,M,A,P)X(S)X(Z)7)  *(122)(L)X(P)(I)XX(W)(I)(SXX(L)XXX(S)X(Z)7)  **IDVSTQTRHATYDDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **IDVSTQTRHATYDDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **ADVSTQTHATYDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **ADVSTQTHATYDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **ADVSTQTHATYDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **ADVSTQTHATYDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **ADVSTQTHATYDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **ADVSTQTHATYDDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **ADVSTQTHATYDENOLOGABITYVEKKSHIZLNITGYPAPFKAVDNINQODEPTI **ADVSTQTHATYDENOLOGABITYDENOLOGABITYNDOLOGABITYDENOLOGAB	<pre>&lt;(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(P)(P,V,X)(P)(P,V,X)(P)(P,V,X)(P)(P,V,X)(P)(P,V,X)(P)(P,V,X)(P,V,Y)(P,V,X)(P,V,Y)(P,V,X)(P,V,Y)(P,V,X)(P,V,Y)(P,V,X)(P,</pre>

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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F)

x{79}(L)x(S)(I)xx(L)(S)(K)xx(V)xxx(A)x(I18)

MSVDANKVKFEFGKNCTGESFEXNKGETVRENNGDKWNDKFMSCLVGSNVRCNIWEHNEI

1: MSVDANKVKFEFGKNCTGESFEXNKGETVRENNGDKWNDKFMSCLVGSNVRCNIWEHNEI
BRA1_BRAFL
                                                                                                                                                                                                                                                                                                                                                        BRA2_BRAFL
                                                                                                                                                                     CAD1_DICDI
                                                                           CAMG_MOUSE
                                                                                                                                                                                                                                                  BSR_BACCE
                                                                                                                                                                                                      ۳..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ck: 7365 len: 448
                                                                                                                                                                                                                                                                                                                                                           ck: 391
                                                                                                                                                                                                      <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F)
x{95}(V)x(S)(P)xx(M)(C)(R)xx(I)xxx(A)x{29}
mktfnisqodlelvevatekitmlxednkhhvgaalftktgeiisavhieaxigrutyca</pre>
                                                                                                                                                                                                                                                     ck: 8425 len: 140 | p33967 bacillus cereus. blasticidin-s
                                                                                                                                                                        ck: 3813 len: 213
                                                                             ck: 283
                                                                                                                                                                                                                                                                                                                                                              len: 440
                                                                              len: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Q17134 branchiostoma floridae (florida
                                                                                                                                                                                                                                                                                                                                                               ; p80492 branchiostoma floridae (florida
                                                                                                                                                                         1 p54657 dictyostelium discoideum (slim
                                                                               1 P49070 mus musculus (mouse). calcium
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#ECAPPAGETYWCZYSTAYLALYXYYZYZYZYZYZYZYZYZYZYZZZZZZZZZZZZZ	<pre> <pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre>
1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{161}(V)x(S)(V)xx(V)(T)(R)xx(L)xxx(V)x{135}	DACX STRSK ck: 4817 len: 291   P39042 streptomyces sp. (strain k15). d-ala
DHBK_MOUSE ck: 4788 len: 312 ! 070503 mus musculus (mouse). putative st	HEQYALSRLHDEKLYLLSABFATRROIDHYCEKACLHPQYVIEANSISAYLELIRR TSLSTLLPAAIATQHDGLKAISLAPPLLERTAVLLRRKNSWQTAAAKAFLHWALDKCAYVGGNESR
NISSGVGVRPWPLYSLYSASKAFVCTFSKALNVEYRDKGIIIQVLTPYSVSTPMTK YLNTSRVTKTADEFVKESLKYVTIGAETCGCLAHEILAIILNLIPSRIFYSSTTQRFLLKQFSDYLKSNISNR	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x{192}(L)x(S)(A)xx(A)(T)(R)xx(I)xxx(C)x{91}  1: MLSRHINYFLAVAEHGSFTRAASALHVSQPALSQQIRQLEESLGVPLFDRSGRTIRLTDAGEVWRQ
1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x[189](L)x(S)(L)xx(S)(S)(X)xx(S)x(101] MEOFILSYGLIVCIVKCVRFSRYLFISFCKALPGSFIRSYGOMAVITGARDGIGKAYSFE	CYNR_ECOLI ck: 4304 len: 299 ! P27111 escherichia coli. cyn operon transcu
DHB3_RAT ck: 3366 len: 306 ! 054939 rattus norvegicus (rat). estradio	1: <(X){1,200}{(,,1,V,M,A,F)X(P,T,S)(L,1,V,M,A,F)XX(L,1,V,M,A,F,Y,M){(,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
NISSGAALRPWPLYSLYSASKAFVYTFSKALSVEYRDKGIIQVLTPYSISTPMTK YLNNKMTKTADEFVKESLKYVTIGAESCGCLAHEIIAIILNRIPSRIFYSSTAQRFLLTRYSDYLKRNISNR	CY2_RHOTE ck: 2620 len: 92 ! P00098 rhodocyclus tenuis (rhodospirillum t
1: MEXITY STATE THE STATE OF TH	1: QAVLYPSIYSILSKSKVRVQELEPVEGAAVPADTKKAEIKEKEHEVITHGLPVPYSSVVQPIVS
	CU04_BLACR ck: 1926 len: 127 ! P80675 blaberus craniifer. cuticle protein
1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(193)(L)x(5)(M)xx(A)(5)(K)xx(Y)xxx(5)x(101) 1: MGDVLEOFFILTGLLYACHACHACVRESRCYLLYWKVLPKSFLRSMGQWAVITGAGDGIGKA GLILNISSGIALFPWPLYSMYGASKAFVCAFSKALOEEYKAKEVIIQVLPYSAVST AMTKYLNTNVITKTADEFVKESLNYVTIGGETGGCLAHEILAGFLSLIPAWAFYSGAFQRLLLTHYVAYLKLNTKVR	1: MNKÄLKÄLGÝLÍTFÝMÍLÍVLIGGALÝTKTGSGÓGGGRÓMPÍCHGRFFPELNPASIIEMSHRFASGI TGAYVRHTESSLAGPNVÞLGSFLNNGLÞYGFHENVÓMGHRAAALLLFÝWIIVAAVH AITSYKDOKGIFWGWISCLIFITLOALSGIMIVYSBLALGFALAHSFFIACLFGVLGYFLLLIARFRYESROS
DHB3_HUMAN ck: 3434 len: 310 ! P37058 homo sapiens (human). estradiol 1	$ < (X)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(G,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y$
A A THOSH MAY HAND HAND HAND A SHANDA I A BANDA DA BANDA DA BANDA HANDA HANDA BANDA HANDA BANDA BANDA BANDA BA	CTAA_BACSU ck: 1522 len: 306 ! P12946 bacillus subtilis. cytochrome aa3 cc
DHAT_KLEPN ck: 846 len: 387 ! Q59477 klebsiella pneumoniae. 1,3-propan  <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W  x{143}(A)x(T)(A)xx(V)(T)(R)xx(V)xxxx(T)x(228)  1:	1
	CTAA_BACFI ck: 716 len: 297 ! Q04443 bacillus firmus. cytochrome aa3 cont
DHAT_CITER ck: 101 len: 387 ! P45513 citrobacter freundii. 1,3-propane  <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W  x{143}(A)x(T)(A)xx(V)(T)(R)xx(V)xxx(T)x(228)  1: MSTRWEDYLVWINFEGPHAISVVGERCKLLGGKRALLVTDKGLRAIKDGAVDKTLTHLREAG INDPLLMLGKPAPLTAATGMDALTHAVEAYISKDANVYTDAAATGAIRLJARNLRQ  INDPLLMLGKPAPLTAATGMDALTHAVEAYISKDANVYTDAAATGAIRLJARNLRQ  AVALGSNILKARENNAXASSLAGMAFNNANLGYVHAMAHQLGGLYDMFHGVANAVLLPHVARYNLIANPEKFADIAEFMGENTDGL	200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX (A)x(S)(V)xx(A)(T)(R)xx(V)xxx(I)x(291) RELAGUSMMTUSRIWHANAESVRPATRARVLQAIQTLNYVP GRDLAEVXQFHMATGDDHYTDLASLLN AKGVRIPQDVAVMGFDNLVGVGHLFLPFLTTIQLPHDIIG
T	CSCR_ECOLI ck: 8969 len: 331 ! P40715 escherichia coli. sucrose operon rep
1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(45){P}x(T)(L)XX(L)(S)(K)XX(V)XXX(V)XXX(D)IDITION: GENDON'S MANY MTRKTITANGGSTANGADISHOTHER GYNUNGERMPAAR AND FIDEL TO ONE SENDON'S MANY	LTELSFNWLGFISAMISNISFTYRSTYSKRAMTDMDSTNIYAYISTIALIVCIPPALIIEGPTLLKTGFNDAIAKVGLVKFVSDLFWV
DFP_STRMU ck: 9135 len: 145   Q54433 streptococcus mutans. dna/pantoth	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,E,Y,W)(Q x(85)(V)x(P)(V)x(F)(S)(R)xx(A)xxx(G)x(301)  MESRYLSRATTLSSETTLINKLHRLEPLANASLPSVKSFGSVSDGGNLVWGRQLRPELCSPVLKKGAS  1: MESRYLSRATTLSSETTLINKLHRLEPLANASLPSVKSFGSVSDGGNLVWGRQLRPELCSPVLKKGAS
MSDTKRDPADLLASIKIDNEKEDTSEVSTKETVKSQPEKTADSIKPAEKLVPKVEEKKTKQED TLEVVQEMGKFTKITSQLIVPDSFEKNKQINAQVIVGTPGTVLDLMRRKLMQLQKI KIFVLDEADNMLDQQGLGDQCIRVKRFLPKDTQLVLFSATFADAVRQYAKKIVPNANTLELQTNEVNVDAIKQLYMDCKNEADKF	CPTR_PEA ck: 5889 len: 402   P21727 pisum sativum (garden pea). triose p
1 $\langle (X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W$ $\times (146)[A] \times (S(I,I,YY(I),TT)(R) \times Y(S(X,Y,I))$	x(54)(P)x(P)x(V)(S)(H)xx(A)xxx(S)x(44)  1: QVGYSGIVSPDGNNIQFTHDFAHSIVLKGPSGIVTSDGKNIQLTAGQASLQAAAPAPPLPVSHY
DBP5_YEAST ck: 2958 len: 482 ! P20449 saccharomyces cerevisiae (baker's	$1 < (X)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q,I,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,$
ANYSTPRHLTKIASSAMKNSTFRTVVKTKAYTAKTVTKTGSIRTMDTWKNTNGLLS SYSGAIGVKTGSGPEAKYCLVFAATRGGKTVIGTVLASTSIPARESDATKIMNYGFAL	CPC1_CANPG ck: 1605 len: 114   P81580 cancer pagurus (rock crab). cuticle

DHBX\_ANAPL

DHC3\_HUMAN

DHCA\_HUMAN

DHCA\_MOUSE

DHCA\_RABIT

DHCA\_RAT

(fruit fl

(baker's

DHKR\_STRCM

1 <\(X)\{1,200\\(L,I,V,M,A,P)X(P,T,S)\(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)\)\(
\text{136}\\
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\text{x\{1}}\text 1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X)(B)}(P)x(Y)(S)(K)xx(Y)xxx(S)x(72) x(188)(P)x(S)(E)xx(Y)(S)(K)xx(Y)xxx(S)x(72) x(188)(P)x(S)(E)xx(Y)(S)(K)xx(Y)xxx(S)x(72) SSCSRVALVTGANRGIGLAIARELCROESGOVVLTARDVARGOAAVQOLQAEGLSPRFHQLDIDDL SSCSRVALVTGANRGIGLAIARELCROESGOVVLTARDVARGOAAVQOLQAEGLSPRFHQLDIDDL TKNEVHEREGWPNSPYGVSKLGVTVLARRLDEKRKADRILVNACCPGPVKTD MDGKDSIRTVEEGAETPVYLALLPPDATEPQGQLVHDKVVQNW 1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x(186)(P)x(S)(A)xx(V)(T)(K)xx(V)xxx(S)x(72) x(186)(P)x(S)(A)xx(V)(T)(K)xx(V)xxx(S)x(72) SSG.IHVALVTGGNNGIGLAIVRDLCRLFSGDVVLTARDVTRGQAAVQQLQAEGLSPRFHQLDIDDL SSG.IHVALVTGGNNGIGLAIVRDLCRLFSGDVVLTARDVTRGQAAVQQLQAEGLSPRFHQLDIDDL SSG.IHVALVTGGNNGIGLAIVRDLCRLFSGDVVLTARDVTRGQAAVQQLQAEGLSPRFHQLDIDDL TKKGVHQKEGWPSSAYGVTKIGVTVLSRIHARKLSEQRKGDKILLNACCPGWVRTD MAGPKATKSPEEGAETTVYLALLPPDAEGPHQQFVSEKRVEQW 1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q X(188)(P)X(S),A)XX(Y)(T)(K)XX(Y)XXX(S)X(72) X(188)(P)X(S)(A)XX(Y)(T)(K)XX(Y)XXX(S)X(72) X(188)(P)X(S)XX(Y)(T)(X)XXX(S)XX(T)XXX(S)XX(T)XXX(T)XXX(T)XXX(T)XXX(T)XXX(T)XXX(T)XXX(T)XXX(T)XXX(T)XX(T 1 <\(X\) \(\lambda\) \(\lambda 1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x(188)(P)x(S)(A)xx(Y)(T)(K)xx(Y)xxx(S)x(72) x(188)(P)x(S)(A)xx(Y)(T)(K)xx(Y)xxx(S)x(72) x(188)(P)x(T)ANNGIGFAIVRDLCRKFLGDVVLTARDESRGHEAVKQLQTEGLSPRFHQLDIDNF 1: SSDRPVALYTGANNGIGFAIVRDLCRKFLGDVVLTARDESRGHEAVKQLQTEGLSPRFHQLDIDNFAKKGVHAKEGWPNSAYGVTKIGVTVLSRIYARKLMEERREDKILLNACCPGWVRTD AKKGVHAKEGWPNSAYGVTKLGVTVLSRIYARKLMEERREDKILLNACCPGWVRTD AKKGVHAKEGWPNSAYGVTLALLPPGAEGPHQQTVQDKKVEPW 1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(125)(L)X(S)(V)XX(M)(T)(K)XX(L)XXX(G)X(131) x(125)(L)X(S)(V)XX(M)(T)(K)XXX(G)X(131) x(T)TATATATATEOTTAKFVALIVEGATISGIGLATARLAALGARTELCARDEERLAQTVKELRGEGE LIXALGLELARTGITVNAVCPGFVETPMAREVREHYAGINQVSEEETFDRITNRVP LGRYVETREVAAMVEYLVADDAAAVTAQALNVCGGLGNY MTOSTSRVÁLÝTĠAŤŠGÍGLÁTÁŘLÍÁAÓGHĽVFI TGITVNAVCÞGYVETÞMAQRVROGYAMAYDTTEEAILTKEQAKIPLGRYSTÞEEVA GLIGYLASDTAASITSQALNVCGGLGNE DHK1\_STRVN ck: 3104 len: 272 č ck: 391 ck: 3202 len: 276 ck: 204 ck: 1426 ck: 3202 len: 9157 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x{114}(L)x(S)(V)xx(M)(T)(R)xx(L)xxx(G)x(131) mnostrylytegatsgiclatarllaagohlvelgartesdylatykalrndgleaeggyldyrg mnostrylytegatsgiclatarllaagohlvelgartesdylatykalrndgleaeggyldyrg ck: 4473 len: len: 312 len: 276 ! 075828 homo sapiens (human). carbonyl len: 276 len: 276 276 261 ! p16152 homo sapiens carbonyl reductase 1 057314 anas platyrhynchos (domestic duck). ! P48758 mus musculus ! P16542 streptomyces violaceoruber. ! P47844 oryctolagus cuniculus ! p47727 rattus norvegicus (rat). carbonyl P41177 streptomyces cinnamonensis. (mouse). carbony1 (rabbit). granati redu [nac cark 1 (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,WX(L,I,V,M,A,F,Y,WX(L))XXX(S)X(B)}
x(147)(V)X(P)(V)XX(A)(T)(K)XXX(S)X(B)S
KKYNNTVLITGGSAGIGLELAKRLLELGNEVIICGRSEARLAEAKQQLPNIHTKQCDVADRS
IEMAPPMYDTGLNQKSRDKQGLTYRGISSEBYVQYFLDGLKEGKQEITNERVEGLR
DATRADYDKLFEQMNTQEN  $\vdash$ 1 (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,189)(L)X(169) x(182)(L)X(S)(A)XX(A)(S)(R)XX(M)XXX(L)X(169) x(182)(L)X(S)(A)XX(A)(S)(R)XXX(L)XX(L)XX(B)SXX(L)XX(B)XXX(L)XX(L)XX(B)SXXX(L)XX(L)XXX(L)XX(L)XXX(L)XXX(L)XXX(L)XXX(L)XXX(L)XXX(L)XXX(L)XXX(L)XXX 1 < (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,30)} \*(30){L},X(S)(M)XX(M)(S)(R)XX(P)XXX(A)X(309) \*(30)\*LLYX(S)(M)XX(M)(S)(R)XX(P)XXX(A)X(309) \*METAPLITAGE AND THE DSBB\_VIBAL DUS1\_HUMAN DUS1\_MOUSE DVR1\_BRARE .. ELAC\_TRIVU ERP2\_YEAST DUS1\_RAT ۳ ۲. ck: 2736 len: 165 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,S)(L)XX(E)(L)XX(E)(S)(E)XX(E)X(I)XX(I)X(I)X(I)X(I)XIX(I ck: 5401 len: 367 ck: 5871 len: 367 ck: 2951 ck: 6443 len: 367 ck: 5524 len: 102 ck: 5386 len: 215 len: 355 ; p28562 homo sapiens (human). dual 1 Q56578 vibrio alginolyticus. ! P28563 mus musculus (mouse). i Q64623 rattus norvegicus (rat). dual spe p35621 brachydanio rerio p39704 saccharomyces cerevisiae Q29143 trichosurus vulpecula

dual specif

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1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,X,I)XXXX(M)X(I18)

1: MNLEGKIALVTGASRGIGRAIAELLVERGATVIGTATSEGGAAAISEYLGENGKGLALNVTDVESI
TVAPGFIETDMTKALNDDQRAATLSNVPAGRLGDPREIASAVVFLASPEAAYITGE
TLHVNGGMYMV
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                                                                                                                                                                        1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C X{171}(P)X(P)(A)XX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)X
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      <u>с</u>
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x{33}(M)x(T)(M)xx(L)(T)(H)xx(P)xxx(P)x{95}
margsmnsgddspmsdinvtplvdvmlvllivemitmpvlthsiplelptaseqtnkqdkqpkdpl</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x{33}(M)x(T)(M)xx(L)(T)(H)xx(P)xxx(P)x{95}
margsmnssddspmsdinvtplvdvmlvllivfmitmpvlthsiplelptaseqankqdkqpkdpl</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ck: 5984
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len:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! O54438 pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! P43713 haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! P95376 neisseria meningitidis. biopolymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! 006434 neisseria gonorrhoeae. biopolymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! Q90257 brachydanio rerio (zebrafish)
! P28861 escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ! 033096 mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! P55336 vibrio harveyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-oxoacyl-[acyl-carr
ferredoxin--nadp
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FIBR\_AGKCO FENR\_SHIFL ck: 7566 len: <(X){1,200}(L,I,V,M,A,F)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{29}(P)x(T)(A)xx(F)(T)(K)xx(L)xxx(G)x{90}
MADMVTGKYTKVQNWTDALFSLTVHAPVLPFTAGQFTKLGLEIDGERVQRAYSYVNSPDNPDL</pre> ck: 1251 203 135 ! P28891 agkistrodon contortrix contortrix P28901 shigella ferredoxin--na

FIMH\_SALTY ck: 6074 len: 335 P37925 salmonella typhimurium.

FLIH\_BACSU ck: 1150 len: 208 ! P23449 bacillus subtilis. flage

1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,Y)(R),XX(V),XXX(L)X{12}

1: MARVEEADRISEQANSHIENIRRQIEQEKNDWAAEKOKLIEEAKAEGFEQGVALGKAEAMKQ
TPFGRVDASVDTQLMQLKDKLLTALEAGAAE

FOS\_AVINK ck: 9324 len: 322 ! P23050 avian retrovirus nk24. p55-v-fos

1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,V)XXX(P)x(252) x(54){P}x(P){P}xx(Y){X}xX(P)x(252) SQDFCTDLAVSSANFVPTUTAISTSPDLQMLVQPTLISSVAPSQNRGHPYGVPAPAPPAAYSR LGAPSPAAABEAFALPLMTEAPPAVPKEPSGSGLELKKAEPFDELLFSAGPREASR SVPDMDLPGASSFYASDWEPLGAGSGGELEPLCTPVVTCTPCPSTYTSTFVFTYPEADAFPSCAAAHRKGSSSNEPSSDSLSSPT

FOS\_CHICK ! P11939 gallus gallus (chicken). p55-c-fo

ck: 7007

len:

367

FOS\_HUMAN ck: 4677 len: 380 . F01100 homo sapiens (human).

1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{99}(A)x(S)(A)xx(Y)Xxx(M)x(265) 1: MMESGENADTEASSSRCSSASPAGDSLSYYISPADSESSMGSPVNAQDFCTDLAVSSANFIPT ALQTEIANLLKEKEKLEFILAAHRPACKIPDDLGFPENSVASLDLTGGLPEVATP ESEEAFTLPLLNDPEPKPSVEPVKSISSMELKTEPFDDFLFPASSRPSGSETARSVPDMDLSGSFYAADMEPLHSGSLGMGPMAT

FTRC\_MAIZE <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W
x[15](V)x(P)(I)xx(A)(T)(R)xx(P)xx(A)x(121)
mrstyttycggluyrplstatigrprrcavraQaAcadasndksvevmrkeseqyarrsnt</pre> ck: 4642 len: 152 P41347 zea mays (maize).

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1 <(x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d
x(65)(L)X(T)(A)XX(I)(S)(K)XX(I)XXX(L)X(294)
m(0KLOISYVIYLETLIVAGPVDLNENGEGKENVEKEGLCNACLWRENTESSRLEAIKIOILSKLRI
kpmkdgtrytgirslkldmnpgtgiwgsidyktylonwikopessigieikalden
ghdlavtfpepgedglfpflevkvtdtpkrsrrdfgldcdehstesrccrypltydfeafgwdwiiapkrykanycsgecefyfloky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q,X,G)(L,I,V,M,A,F,Y,W)(Q,X,G)(L,I,V,M,A,F,Y,W)(Q,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,G)(L,X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x(65)(L)X(T)(A)XX(L)X(X)X(L)X(294)
M(KLOLCYVIYLEMLIVAGPVDLNENSEQRENVEREGLCNACTWRQNTKSSRIEAIKIQILSKLRI
MOKLOLCYVIYLEMLIVAGPVDLNENSEQRENVEREGLCNACTWRQNTKSSRIEAIKIQILSKLRI
KPMKDGTRYTGIRSLKLDMNPGTGIWQSIDYKTYLQNWLKQPESNLGIEKALDEN
KPMKDGTRYTGIRSLKLDMNPGTGIWQSIDYKTYLQNWLKQPESNLGIEKALDEN
KPMKDGTRYTGIRSLKLDMNPGTGIWQSIDYKTYLQNWLKQPESNLGIEKALDEN
KPMKDGTRYTGIRSLKLDMNPGTGIWQSIDYKTYLQNWLKQPESNLGIEKALDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDF8_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDF8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDF8_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDF8_PAPHA
                                                                                                                                                                                                                                         GLPB_PANTR
                                                   GPDA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDF8_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 1814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ck: 9403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ck: 2293 len: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 1463 len: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 1805 len: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ck: 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 1548 len: 375
                                                                                                                                                                                                                                            ck: 149 len: 123
                                                                                                                                      (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(D,X,(B)(Y)x(P)(Y)xX(F)(S)(R)xx(P)xxx(I)x(27)
x(80)(Y)x(P)(V)xx(F)(S)(R)xx(P)xxx(I)x(27)
MYGKIIFVLLLSEIVSISASSTIEVAMHISTSSSVIKSYISSQINDKHKGDIYPATLGAHEVSE
MYGKIIFVLLLSEIVSISASSTIEVAMHISTSSSVIKSYISSQINDKHKGDIYPATLGAHEVSE
<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    len: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i 008689 mus musculus (mouse). growth/differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 018836 bos taurus (bovine). growth/differen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! 014793 homo sapiens (human). growth/differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i 018828 papio hamadryas (hamadryas baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! 018831 sus scrofa (pig). growth/differenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 018830 ovis aries (sheep).
                                                                                                                                                                                                                                                         ! Q28914 pan troglodytes (chimpanzee).
                                                                      ; p37606 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               035312 rattus norvegicus (rat). growth/dif
                                                                               coli.
                                                                                   glycerol-3-phosphi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth/differen
                                                                                                                                                                                                                                                                               glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x(68)(L)x(T)(A)xx(A)(S)(R)xx(L)xXx(P)x(255)

MNORNASMTVIGAGSYOTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLEDVPFFDTL
RVYSNPDFIGVOLGGAVKNVIAIGAGMSDGIGFGANARFALLTRGLAEMSRLGAAL
RVYSNPDFIGVOLGGAVKNVIAIGAGMSDGIGFGANARFALLTRGLAEMSRLGAAL
GADPATFMGMAGLGDLVLTCTDNOSKNRRFGMMLGOGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEMPITEEIYQVLYCGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X)](P)xx(Y)(S)(K)xx(M)xxx(L)x(183)
x(97)(P)xx(P)(P)xx(V)(S)(K)xx(M)xxx(L)x(183)
MHRRISHSCREDOKPVMDDORDLISNNEQLEMGARPGAPESKCSRGALXTGFSILVTLLLAG
WKVFESWMHHWLLFEMSRHSLEOKPTDAPPKVLTKCQEEVSHIPAVPHGGSFRPKCD
WKVFESWMHHWLLFEMSRHSLEOKPTDAPPKVLTKCQESUSHIPAVPHGGSFRPKCD
WKVFESWMHHWLLFEMSRHSLEOKPTDAPPKVLTKCQESUSHIPAVPHGGSFRPKCD
WKVFESWMHHWLLFEMSRHSLEOKPTDAPPKVLTKCQESUSHIPAVPHGGSFRPKCD
WKVFESWMHHWLLFEMSRHSLEOKPTDAPPKVLTKCQESUSHIPAVPHGGSFRPKCD
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 <(X)[1,200](L,1,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,170)(L)xx(L)(T)(L)xx(L)(T)(R)xx(A)xx(A)x(173)
x(170)(L)x(T)(L)xx(L)(T)(R)xx(A)xxx(A)x(173)
mstentlyadlarenvenlypyGsarrigengdywlnanefptavefgltogtlnrypecop
grgkaivyadeayiefcoatltgwlyfyphlyilrtiskafalaglrogftlane
evinlllkviapyplstpyadiaagalcpoginamrdryagtvoergylvnalogtacvehyfdsetnyilarftasssyfkslw
                                                                                                                                                                                                                         GPRD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HG2A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIS8_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPRD_RAT
                                                                                                                                                                                                                                                                                                                                                                         HISQ_ECOLI
                                                                                                                                                         HMPH_HUMAN
                                                      1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 2863 len: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 9949 len:
                                                                                                                                                                                                                                                                                                                                                                                      ck: 7651
                                                      <(X){1,200}(L,I,V,M,A,P)X(P,I,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,I,03)(P)X(P)X(P)X(P)X(I)XXX(P)X(ISI)
x(1.03)(P)X(Y)(V)XX(Y)(I)XXX(P)X(ISI)
xQYPHPGPAAGAVGVPLYAPTPLLQPAHPTPEYIEDILGRGPAAFTPAPTLPSPNSSFTSLVS</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 len: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     len:
                                                                                                                                                                                                                                                                                                                                                                                      len: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359
                                                                                                                                                                               270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i P35411 rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p50200 clostridium sordelli.
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; p04233 homo sapiens (human). hla class

p10369 salmonella typhimurium.

1 P52094 escherichia coli.

histidine trans

1 Q03014 homo sapiens

(human).

homo

sapiens

(human).

probable

g

(rat). probable

ă

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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(103){V)X(P)(V)X(W)(S)(H)XX(L)XXX(S)X(193)

TLEMERLIQAKGGSESQNVEELLNLLPKRGPQAFDAFCEALRETRGGHLEDLLLTTLSDIQHILPPL
DQTAQEMQEKLQNFAQLPAHRVTDSCIVALLSHGYEGGITGVDGKLLQLGEVFELF
DNANCPSLQNKPKMFFIQACRGDETDRGVDQQDGKNHAQPPGCEESDTVKEELMKMRLPTRSDMICVYACLKDNAPIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(25)(P)X(T)(M)XX(L)(S)(R)XX(L)XXX(G)X(258)

1: AKVETKDVMEQFNLELISGEEGINRPITMSDLSRPGIEIAGYFTYYPRERVQLLGKTELSFFEQLF
VEIRQEDQDTLYGNAPELIEHLLEIRGLGINVYMILFGAGAVRSNKRITIVMNLEL
WEQGKOYDRLGLEEETMKIIDTEITKLTIPVRPGRNLAVIIEVAAMNFRLKRMGLNAAEQFTNKLADVIEDGEQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,A,F,Y,M,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,M,X,X)(C,I,V,X,X,X)(C,I,V,X,X)(C,I,X,X)(C,I,X,X)(C,I,X,X)(C,I,X,X)(C,I,X,X)(C,I,X,X)(C,I,X,X)(C,I,X,X)(C
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SQCSPSPASQEDLESEISEDSDQEVDIEGDKSYFNAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAA2_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [AA1_WHEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ck: 4393 len: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ck: 8616 len: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \begin{array}{l} <\langle (X)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X\{91\}(A)x(S)(I)xx(V)(C)(R)xx(I)xxx(A)x\{17\} \\ \\ \times (91PMMCYPGQAFQVPALPGCRPLLKLQCNGSQVPEAVLRDCCQQLADISEMPRCGALYSMLDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ck: 4073 len: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x(91](A)x(S)(I)xx(V)(C)(R)xx(I)xxx(A)x(17)
SGPWMCYPGQAFQVPALPACRPLLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSMLDSM</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ck: 3320 len: 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 8827 len: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <(X) [1, 200] (L, I, V, M, A, P)X(P, T, S) (L, I, V, M, A, P)XX(L, I, V, M, A, F, Y, W) (C
x { 90 } (A)x(S) (V)xx(V) (C) (K)xx(I)xxx(S)x{17}
SGPWSWCNPATGYKVSALTGCRAMVKLQCVGSQVPEAVLRDCCQQLADINNEWCRCGGLSSMLF</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 4825 len: 123
<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(D
                                                                                                7697 len:
                                                                                                      207
                                                                                           ! P10822 psophocarpus tetragonolobus (goa be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! P55215 rattus norvegicus (rat). caspase-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ! P01084 triticum aestivum (wheat). alpha-am;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ! P01085 triticum aestivum (wheat). alpha-am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! P16430 escherichia coli. formate hydrogenl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! P28153 rhizobium leguminosarum (biovar vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! P01083 triticum aestivum (wheat). alpha-am
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 $\begin{array}{c} \textbf{x}\{69\}(\textbf{V})\textbf{x}(S)(\textbf{F})\textbf{xx}(\textbf{V})(S)(\textbf{K})\textbf{xx}(\textbf{F})\textbf{xx}(S)\textbf{x}\{122\}\\ \textbf{1:}\\ \textbf{MKSTTFLALFLLSAIISHLPSSTADDDLVDAEGNLVENGGTYYLLPHIWAHGGGIETAKTGNE}\\ \textbf{RNGNRRLVVTEENPLELVLLKAKSETASSH} \end{array}$ 

ck: 9024 203 P72002 mycobacterium tuberculosis.

ck: 2843 len: 332 ! P39343 escherichia coli. l-idonate

1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)
x[10](I)x(T)(L)xx(V)(T)(K)xx(V)xxx(I)x[306]
x[10](I)x(T)(L)xx(V)xxx(I)x[306]
mrnhrisiqdiatlagyrkmtysryirspkkvaketgeriakimeeinyipnrapgmllnaqs
krvrhkilyigskddtrderoxdamlhnisplrnneraissihigndlmrd
alsanpdldgyfctnddiamgalllcrernlavpeqisiagfhgleigrqmipslasvitpredigrmaaqmllskiknndhnhn

ck: 6528 len: 131 ! P09182 escherichia coli. colicin n immun

ck: 6434 len: 424 ! P18642 salmonella typhimurium. dqmi prot

181

P31608

sagittaria

ck: 4153 len: 342 i Q55274 synechocystis sp.

μ

ck: 3484 len: 254 ! P50842 bacillus subtilis.

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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q
x(143)(A)X(P)(A)X(Y)(P)(R)XXY(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)X
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x{42}(V)x(T)(L)xx(V)(T)(K)xxx(L)x(144)
mpdeptgsadplisteeaggagepnapapprrlrmlsvavvvltldivtkvvavqllepgqpvs1
FGFDFDTVGRRHADGDTVGRRKADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,E,Y,W)(d)
x(157)(L)X(P)(L)XX(P)(T)(R)XX(L)XXX(A)X(257)
MDLLSDIEKQLOKATAQAELIALSGELDSTYLLSLEFAKLCQKOPHLPPLSIRAIHIHHGLSPNADS
LNWITDESNEDNRYDBNFLRNBLIEDLERBWAHFDLAVORSAOHGEBOOOLINDLL
ERBKLOKTORNSTARNDLAENGLENGERBOOOLINDLL BAKEEANPQFQLVNKVIRRYQDSLYLTKPFSG
SEIFTEHCQIKNQFKLCQFRQYSLAKQTALLRMWLAENGLEMPSKRQLTGLINDVIFAKEEANPQFQLVNKVIRRYQDSLYLTKPFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q
x(196)(L)X(T)(M)XX(Y)(T)(K)XX(L)XXX(I)X(108)
MARKITALIGSGNIGGILAHLAGLKELGDIYLFDIADGIPQGKGLDISQSSPVEGFDVNLTGASDY
DTMVPLARYSTYGG.IPLIDLYTMGWYKEBLEEIIQRTRODGGAEIYGLLKTGSAYY
APAASAIEMAESYLKDKKRYLPCAAHLSGQYGVKDMYYGVPTVIGAGGVERIIEIDLNKTEKEAFDKSVGAVAGLCEACINIAPALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------
1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x{83}(L)x(P)(A)xx(A)xxx(T)x(137)
MTKNIVNTALVLVGAGSLLTGCNFEODETNCFVQESPSWAVKYDVVDSPKDANGDECTTTAPLVEL
YVWRAVWPPAPCDTASTEPAENCGVGSGLNPEFAVVCQPTSATGTTGYCVPAGDIP
SFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d)
x(141](P)x(T)(P)xx(T)(x)(P)xx(A)xxx(A)xx2(40)
x(141)(P)x(T)(P)x(T)(S)(P)xx(A)xxx(A)xx2(A)x(240)
MQGISVTGLVKRGMVRSVFDTIDGIDGLGEGLASVTVTLDKLAAIQPQLVALLPDEIASQQINRE
AATEKDIQDGATYDLLIAGIAALSLILLIMMITTRSLVAALVIVGTVALSIGASFG
LSVLVWQHLLGIQLYMIVLALAVILLLAVGSDYNLLLISREKEEIGAGLNTGIIRAMAGTGGVVTAAGLVFAATMSSEVFSDLRVLGQ
LSVLVWQHLLGIQLYMIVLALAVILLLAVGSDYNLLLISREKEEIGAGLNTGIIRAMAGTGGVVTAAGLVFAATMSSEVFSDLRVLGQ
                                                                                           MAUF_PARDE
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                   (african
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NUOJ_ECOLI
                                                                                                                   NUZM_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>:</u>:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
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                                                                                                                                                                                                                                                                                 Η.
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<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x(8){M)x(P)(L)xx(L)(T)(H)xx(L)xxx(I)x(96)
MSAVPLTRMLPLRFLTHLLLLSFIPLYFCMEFSEDARNIEKIRRGNQWAIGHFMGKKSLQD</pre>
ck: 8799 len:
      229
      1 P09135 klebsiella
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ck: 7169 len: 271

Q00278 aspergillus

parasiticus.

<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x(8){L)x(S)(I)xx(A)(T)(K)xx(L)xxx(S)x{48}
SELSPSELESITLATKVLLLSSSELWIRASYPRERYDOLMHLLWKNFLPLTLAMCLWHTS</pre>

<(X){1,200}{(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x(M)x(T)(I)xx(L)(S)(K)xx(M)xxx(I)x(150)
wMLTIIMLSKIPMSSLISHILTIYLNNIFNSPSHLLIYLISYSIYMSLMMFTMCSMNSLLILM</pre>

ck: 6545 len: 167

! P34857

apis mellifera

ligu**stica** 

ck: 3961

len:

263

1 P40915 neurospora

nadh-ubiquinon

ck: 9647 len: 215

P42027 brassica oleracea

<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{1,3}(L)x(T)(L)xx(I)(T)(H)xx(P)xxx(L)x{155}
mefafyicgliailatlrvittinpvhallyliisllaisgvefslgayfagaleiivyagai</pre>

 $\times \{1,200\} (L,I,V,M,A,P) \times (P,T,S) (L,I,V,M,A,P) \times (L,I,V,X,M,A,P) \times (D,X,Y,M,A,P) \times (D,X,Y,A,P) \times (D,X,Y,A,P)$ 

P19968

neurospora

crassa.

nadh-ubiquinon

7750

ck: 2909

len:

184

P33605

escherichia

coli.

ck: 6471 len: 72

! P24968 coturnix

coturnix

ck: 1655 len: 214

! Q31651 anser

caerulescens

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1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X)(T,Y,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X)(T,Y,M,A,P)XX(I)X(T,Y,M,A,P)XX(I)X(T,Y,M,A,P)XX(I)X(T,Y,M,A,P)XX(I)X(T,Y,M,A,P)XX(I)X(T,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(3)(L),X(S)(V)xx(L)(S)(K)xx(I)x(X)(Z)(S)

1: MENLLSVKDLSKQQILDLLALAKAVKANPABEYSQALAGKSIVTIYEKPSLRTRVTEDIGIHKLGGH
CPRGSSPDAQIVKQAMALAEISGGKINYTUNLDALVDYDY IXGDTWYSWGDDTPLA
QVKEKYMPYQINKALLMRTGIKHVLHCQPAHRELEITSEVMDGEHSLIFDQAENRMHAQNAVLLTLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x(185)(I)x(S)(I)x(I)(R)xx(M)xxx(L)x(105)
1: MLKFILRRCLEAIPTLFILITISFEMMILAPGSPETGERALPPEVLANIEAKYHLNDPIMTQYFSY
MVALSLAYIASIARITRGSMIEVLHSNEINTARAKGLPMARIIFRHALKPALLEVL
SYMGPAFVGIITGSMVIETIYGLPGIGQLFVNGALNRDYSLVLSLTILVGALTILFNAIVDVLYAVIDPKIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *(185)(1)x(5)(1)x(7)(8)xx(M)xxx(1)x(105)

MLKFILIRCLEAIPTLFILITISFFMMRLAPGSPFTGERTLPPEVMANIEAKYHLNDPIMTQYFS
MVALSLAXIASIARITRGSMIEVLHSNFIRVARAKGLPMRRIILKHALKPALLPVL
SYMGPAFVGIITGSMVIETIYGLPGIGQLFVNGALNRDYSLVLSLTILVGALTILFNAIVDVLYAVIDPKIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x[181](L)X(P)(A)XX(W)(S)(R)XX(P)XXX(L)X(176)
MESFAVAAAQLEPHFAPLSWIGSVVDKYDEDMHLISPYWQFPAMDPIWAKILTAYMIMIGMISWC
SIWCLAPAFGWSRYVPEGNLTSCOIDYLERDWHPRSYLLFYSIFVYY;PLFLLCYS
YWFIIAAVSAHEKAMREQAKKMNVKSLRSSEDAEKSAEGKLAKVALVTITLWFWAWTPYLVINCMGLFKFEGLTPLNTIWGACFAKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x(179)(L)X(P)(V)XX(W)(S)(R)XX(P)XXX(L)X(176)
MERYSTPLIGSSFAALINGSVTDKVTPDMAHLVHPYWNQFPAMEPKWAKFLAAYMVLIATISWCGN
WTLAPVFGWSRYVPEGNLTSCGIDYLERDWNPRSYLIFYSIFVYYLDJETLYSYW
FIIAAVSAHEKAMREQAKKMNVKSLRSSEDADKSAEGKLAKVALVTISLMFMAWTPYTIINTLGLFKYEGLTPLNTIWGACFAKSAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
maskvytgvykttaggvvpvsqkytvqsvgvwerirrafaidpnrsngvplvpynrnpspgsldpi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPS1_DROPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTC_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ck: 7498 len: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ck: 4358 len: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ck: 9791 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ck: 4920 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ck: 9240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 7241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      len:
                                                                                                                                                                                                                                                                                               341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! P96172 vibrio sp. (strain 2693). ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! P08005 salmonella typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! P28678 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! P06002 drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! P22269 calliphora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! P31317 schizosaccharomyces
                                                                                                                                                                                                                                                                                   P31228 bos taurus (bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               escherichia coli. oligopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pseudoobscura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vicina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligopeptid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
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                                                               PLEK_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEX3_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLAS_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PI7A_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETP_RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P2Y6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OXDD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>..</u>
                                                                                                                                                                                                                         ck: 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ck: 804
                                                               ck: 1536
```

len:

263

Q40708 oryza

sativa

! P16678

len:

350

1 P08567 homo

sapiens

126

P21697

(strain

```
GGTRQKGDWNLSPDAEISKEILSRCCALEPSLRGAYDLREKVGLRPTRPSVRLEKELLAQDSRRLPVVHHYGHGSGGIAMHWGTA
                                                                                                                                                                                                                        <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{68}(L)x(S)(V)xx(V)(T)(K)xx(L)xxx(L)x{82}
MADTGAPGGETLLFLTDEQLRKGIEAMFFAYRGFTADPDRILDQHDYGRAHHRAIHFINREPG</pre>
                                                                                                                                                                                                                                                                                                                                                                                     ck: 7545 len: 328
                                                                                                                                                                                       ck: 166
                                                                                                                                                                                                                                                                        ck: 1875 len: 166 ! P31078 rhodobacter capsulatus (rhodopseu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ck: 7167 len:
                                                                          ck: 2829
                                                                          len:
                                                                                                                                                                                      len: 441
                                                                          246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341
                                                                                                                                                                                                                                                                                                                                                                                    ! Q15077 homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! Q99489 homo sapiens (human). d-aspartate
                                                                          ! P14697 alcaligenes
                                                                                                                                                                                      ! P28795 saccharomyces
                                                                                                                                                                                     (baker's
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FKLEFGRDSSGRIRLGDEVSPDTCRLWDMETGEPLDKDIFRRGEEGVVGAYRRVAR
MILDDEDIERWNVEL
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1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d
x(151)(P)x(S)(V)xx(L))xxx(V)xx(209)
MDVLAEANOTFALMILKTIGKDNSKNVFFSPMSMSCALAMYYMGAKGNTAAOMAQILSFNKSGGGG
DKENTEERLFKVSKNEEKPVOMMFKOSTFKATVIGETFTOLIVLPYVGKELNMIIN
LPDETTDLRTVEKELTYEKFVEWTRLDMMDEEEVEVSLPRFKLEESYDMESVLRNLGMTDAFELGKADFSGMSOTDLSLSKVVHKSFY 1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d)
x{111}(L)X(S)(A)XX(L)(S)(L)XX(Y)XXX(P)X{172}
MKHKDLIGKASIHKNKTIAVAHAEDEBYIRAVKHAAEHLSARFLLTGDSKKLNELTSSMOGHQVEI
TVNPKMEATUNAAALAOMYKRGQIKGCIVOGPLALDNAVSCIAAAQKKISGDVAGN
PDILLVPTIEAGNILYKSLIYFAKASVAAVITGAKAPIALTSRADSAENKLYSTALAICASEEYTH 1 <(x)(1,200)(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d)
x(149)(A)X(T)(V)X(L)(T)(K)XXX(L)XXX(1)X(209)
MDDLCEARGTFA\SLFKILGEBDNSRNVEESPMSISSALAMVEMGAKGSTAAQMSQALCLYKDGDI
KYTRGMLFKTNEEKKTVQMMFKEAKFKMGYADEVHTQVLELPYVEELLAMVILLPD
EXTRGMLFKTNEEKKTVQMMFKEAKFKMGYADEVHTQVLELPYVEELLAMVILLPD
DNTDLAVVEKALTYEKFKAWTNSEKLTKSKVQVFLPRLKLEESYDLEPFLRRLGMIDAFDEAKADFSGMSTEKNVPLSKVAHKCFVEV ! P35237 homo sapiens (human). placental 1 026272 methanobacterium ! P50452 homo sapiens probable pulmonary (pea cytoplasmic phosphat surf thro 1 <(x)(1,200)(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,F,Y,W,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,X,M,A,F, 1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,M,X,P)XX(L,I,V,M,A,F,Y,M,X,P)XX(L)XX(L)XX( PYRB\_ECOLI PYRB\_MYCTU PYRB\_PYRHO PYRB\_PYRAB PYRB\_SALTY PYRB\_SERMA PYRB\_VIBS2 PYRZ\_BACSU ck: 3945 ck: 9304 len: 308 ck: 1547 len: 319 ck: 2583 len: 310 ck: 9980 len: ck: 4826 ck: 2658 ck: 5096 len: 310 310 308 305 256 1 P71808 ! P77918 pyrococcus abyssi. aspartate ! P00479 escherichia coli. aspartate i 058451 pyrococcus ! P19910 serratia marcescens. aspartate P08420 i P96174 vibrio sp. (strain ! P25983 mycobacterium tuberculosis. salmonella bacillus subtilis. horikoshii. typhimurium. aspartate

PTI6\_HUMAN

ck: 300

len: 376

PTI8\_HUMAN

ck: 4145 len:

374

PUR7\_METTH

ck: 5550

len:

248

H

<(x){1,200}(L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F,Y,W)(C)
x{87}(M)x(P)(1)xx(1)(T)(R)xx(A)xxx(I)x{145}
mdvkidgplysgkakdvlltddpeivavrerdditagdgekkdtlemkgyynsvisakifevleea</pre>

```
1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,V,W)(C
x(11){A}x(1)(A)x(P)(S)(R)xx(A)xxx(A)x(2)4}
x(11)Ax(A)x(P)(A)xx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(A)xxx(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLYA_MYCPO
                                                                                                                                                                                                                                                                                                                     PSPB_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PME_ASPTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PME_ASPAC
PTB_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ck: 8743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ck: 2447
                                                                                                                                                                                                                                                                                                                                ck: 7861 len: 79
                                                                                                                                     <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x(27)(A)x(T)(V)xx(V)(C)(H)xx(P)xxx(G)x{35}
rpipipycwllrtlikkiQaVipkGVLAMTVAQVCHVVPLLVGGIIQQLVIEYSVILXTDTLLC</pre>
          ck: 158
          len: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           len: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           len: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! Q12535 aspergillus aculeatus. pectinestera
                     ! P54530 bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | P17872 aspergillus tubingensis.
                                                                                                                                                                                                                                                                                                                                     i P15781 bos taurus (bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q12639 mycosphaerella pinodes
```

RBSK	RBS3_SO	RBS2	1 PEGY 1:	1 1: PGF RBS1_SOLTU	RBS1_LYCES  1  PEGF  RBS1_PETSP	RBS0_SOLTU 1 1 1:	RBCR_CHRVI  1  GERAISLARLAEETFVMREE SGLGLSVVSLHTIELELETR	1: NESEVLDNVAFTRAHNS ELAARONHLGLFLRMLQ	ESETSYVKVCLDGPVFKAQEVAL RA51_DROME c
_SCHPO ck: 3214 len: 318 ! O60116 schizosaccharomyces pombe (fission y <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F;Y,W)(C x {169}(P)x(P)(A)xx(L)(S)(H)xx(I)xxx(A)x{133}	SOLTU ck: 4433 len: 181 ! P32764 solanum tuberosum (potato). ribulose <(X){1,200}(L,I,V,M,A,P)X(P,T;S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{5}(V)xX(S)(A)xx(A)(T)(R)xx(V)xxx(S)x{160} MASSIVSSAAVATRSNVAQASNVAPFTGLKSAASFPVTKKNNNVDITSLASNGGRVRCMQVWPPIN	_LYCES ck: 4535 len: 180 ! P07179 lycopersicon esculentum (tomato). ri <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(5)(1)X(S)(A)XX(A)(T)(R)XX(V)XXX(S)X(159) xASSVISSAAVATRSNVTQASMVAPFTGLKSSATFPVTKKQNLDITSIASNGGRVSCMQVWPPINK	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C     x(5)(I)x(S)(A)xx(A)(T)(R)xx(V)xxx(G)x(160)     MASSVISSAAVATRINVTQAGSMIAPFTGLKSAATFPVSRKQNLDITSIASNGGRVRCMQVWPPIN</pre>	<pre>&lt;(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(5)(I)x(S)(A)xx(A)(T)(R)xx(V)xxx(S)x{159} massvissaavatrinvaqasmvapenglksavsepvsskqnlDiTsIasnggrvqcmqvwpPygk massvissaavatrinvaqasmvapenglksavsepvsskqnlDiTsIasnggrvqcmqvwpPygk massvissaavatrinvaqasmvapenglksavsepvsskqnlDiTsIasnggrvqcmqvwpPygk massvissaavatrinvaqasmvapenglksavsepvsskqnlDiTsIasnggrvqcmqvwpPygk massvissaavatrinvaqasmvapenglksavsepvsskqnlDiTsIasnggrvqcmqvwpPygk</pre>	CES ck: 5240 len: 181   P08706 lycopersicon esculentum (tomato). ri <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(5)(Y)X(S)(A)XX(A)(T)(R)XX(Y)XXX(S)X(160) MASSIVSSAAAATRSNVAQASMVAPFTGLKSAASFPVTKKNNNVDITSLASNGGRVRCMQVWPPIN  TSP ck: 2967 len: 180   P04714 petunia sp. (petunia). ribulose bisp	<pre>LTU ck: 4699 len: 181 ! P10647 solanum tuberosum (potato). ribulose &lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C</pre>	RBCR_CHRVI ck: 4295 len: 302   p25544 chromatium vinosum. rubisco operon t  (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,I)XX(Y)(S)(R)XX(Y)X(203)  (83){(L)XX(Y)(S)(R)XXX(Y)X(203)}  1: MHYSLROLRVEENVARHNSYTRALELHLSQPAVSMQVRQLEDEIGLSLFERLGKQVVLTEAGREV GERAISLARLAEETFVMREEGSGTRQAMERFFSERGQTIRHGMOMTRNEAVKQAVR SGLGLSVVSLHTIELELETRRLYTLDVEGFPDRRQWYLVYRRGKRLSPAAGAFREFVLSBAARMHCRLG	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(CX)(V)xx(A)(T)(K)xx(L)xxx(P)x(275)  * * * * * * * * * * * * * * * * * * *	/FKAQEVAL _DROME ck: 2533 len: 336 ! Q27297 drosophila melanogaster (fruit fly).
1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W	x(126)(L)x(T)(L)xx(L)(S)(K)xx(T)x(85) x(126)(L)x(T)(L)xx(L)(S)(K)xx(T)x(85) x(126)(L)x(T)(L)xx(L)(S)(K)xx(T)x(E)x(S)(S)(S)(S)(S)(S)(S)(S)(S)(S)(S)(S)(S)(	1: GLTVAWCLPKPLPKGT NAVFSTYYALAVSAVT RHO7_HU	RHL_MACMU ck: 4371 len: 416 ! Q28849 macaca mulatta (rhesus macaque).	RFBB_NEIGO ck: 5086 len: 346 l p3776l neisseria gonorrhoeae. dtdp-gluco  (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,M  x{160}(P)x(S)(P)xx(A)(S)(K)xx(A)xxx(V)x{170}  MQYEGKRILIVTGGAETGABAVVRHIIONTRDSVVNLDKLTYAGNLESLTDIADNPRYAFEQV  AWQRTYRLPSIVSNCSNNYGPRKJLIPHMIANALSGKPLPVEGDGAQIRDHUF  VEDHARALYQVVTEGVVGETYNIGGHNEKTNLEVVKTICALLEELAPEKPAGVARYEDLITFVQDRPGHDARYAVDAAKIRRDLG  VEDHARALYQVVTEGVVGETYNIGGHNEKTNLEVVKTICALLEELAPEKPAGVARYEDLITFVQDRPGHDARYAVDAAKIRRDLG	REP2_YEAST ck: 6596 len: 296 ! P03872 saccharomyces cerevisiae (baker's (x) {1,200} {L,I,V,M,A,P}X(P,T,S) {L,I,V,M,A,P}XX(L,I,V,M,A,F,Y,W X) {1,200} {L,I,V,M,A,P}XX(I)XXX(A)X{264} {1,200} {MDIETAKNLTVKARTAYSVMDVCRLFIEMIAPDVDIDIESKRKSDELLFPGYVIRPMESLTT LVSVVTQLLTLVPPDRQAALIGDLEIPESLKDIFNSFNELAAENRLQQKKSELEGR TEVNHANTNEEVPSRRTRSRDTNARGAYKLONTITEGPKAVPTKKRRVATRVRGRKSRNTSRV	REHY_TORRU ck: 4850 len: 218 ! P52574 tortula ruralis (moss). rehydrin.  1 <(X){1,200}{L,I,V,M,A,P}X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W X{160}{L}X(S)(L)X(S)(L)XX(A)(S)(K)XX(I)XXX(A)X{42}  1 MGGWALGDLYDDIQADSTMGHIKVRDYCKDGWTIIFSHPGDYPPVCTTELGKIAAYNPEFEK WQKGEPVVISPSVSDEKAKQMFPQGWETVNLPKALRMTFVD	REG5_DROME ck: 7903 len: 298   Q94913 drosophila melanogaster (fruit fl  <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W  X{131}(A)X(S)(L)XX(L)(T)(R)XX(L)XX(A)X(151)  WITAAKVIIACCLUGAFHIQISSSSAIPIMEFUTRNEKMSHLYSTFAQLVSVHCKSTAAVGGL DKAYGYGPQSSSELPVAAALTSEPSKFLTGPLVIKVRPDGSPVEEDKMMPLPRDE DLPYLSSWSGRRSAQQAPQDRHNQLLKAAALKLHPAERPPATPPDAEASVPPATGVRSRSEDPQA	RBS_MUSAC ck: 2518 len: 180 ! 024045 musa acuminata (banana). ribulose  1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W	1: MINIVVLGSMNTDLVMRTKICPSGGETIHGEPDGFSTGNGGKGANQAVAVARLSNPADTKVSM HDMISYCAYLVPNEHEAAIILNQADSPATLENVDAYASKLLSFGYRKAVIITLGSQ GAYYKSANGESALVSACKVKAVDTTAAGDTFIGAFSNSIAHGQPLKDSLEFAAKCSAITYQRKGAASSIPSLLEVDGSFNLKKNT

1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,I) x(160)(P)x(S)(P)xx(A)(x)(X)x(A)xx(V)x(I70) x(100)x(S)(P)xx(A)(X)(X)x(A)xx(V)x(I70) x07EGKKNLIVTGGAGEIGSAVVRHIJONTROSVVNLIDKLTYAGNLESLTDIADNPRVAFEQYAWQRTYRLPSIVSNCSNNYGPRQFPEKLIPLMILNALSGKPLPVYGDGAGIRDWLF VEDHARALYQVVTEGVVGETYNIGGHNEKTNLEVVKTICALLEELAPEKPAGVARYEDLITFVQDRPGHDARYAVDAAKIRRDLA
RFBB_NEIGO ck: 5086 len: 346   p37761 neisseria gonorrhoeae. dtdp-gluco
1 <(x){1,200}(L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F,Y,N,X,Y,Y,M,A,P)XX(L)XXX(A)X{264} x{16}(A)X(S)(Y)XX(Y)(C)(R)XX(I)XXX(A)X{264}  1: MDDIETAKNLTVKARTAYSVMDVCRLFILADDVDIDIESKRKSDELLFPGYVIRPMESLTY LVSVVTQLLTLVPPDRQAALIGDLFIPESLKDIENSYNELAAENRLQQKKSELLEGR TEVNHANTNEEVPSRRTRSRDTNARGAYKLQNTITEGPKAVPTKKRRVATRVRGRKSRNTSRV
REP2_YEAST ck: 6596 len: 296 ! P03872 saccharomyces cerevisiae (baker'
1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,I) x{160}(L)x(S)(L)xx(A)(S)(K)xx(I)xxx(A)x{42}
REHY_TORRU ck: 4850 len: 218 ! P52574 tortula ruralis (moss). rehydrin
1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,N,X,E,Y,N,E)X(L)XX(L),Y(M,X,E)XY(L)XX(L)XX(L)XX(L)XX(L)XX(L)XXX(A)X{151}  NITAKKVILACCLICAFHOISSSAIPWEFLTRNEKMSHLYSTFAQLVSVHCKSTAAVGGI DKAYGYGPQSSSELPYAAALTSEPSKRFLTGPLVIRVRPDGSPVEEDKMMPLPRDB DLPYLSSWSGRRSAQQAPQDRHNQLLKAAALKLHPAERPPATPPDAEASVPPATGVRSRSEDPQA
REGS_DROME ck: 7903 len: 298   Q94913 drosophila melanogaster (fruit f
1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,V,V,V,V,V,V,V,V,V,V,V,V,V,V,V,V,V,V
RBS_MUSAC ck: 2518 len: 180 ! 024045 musa acuminata (banana). ribuloso

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RIPA_LUFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RS13_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RR8_MARPO
                                                                                                                                                                                                                                                                                        RUVB_THETH
                                                                                                             S27A_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                             RS8_SYNY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x(73)(1)x(T)(L)xx(I)(S)(K)xx(L)xxx(S)x443}
mgndTianmitSirnanLgKIKTVQVPATNITRNIAKILFQEGEIDNFIDNKQNTKDILILNLKYQ</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 6002 len: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <(x)(1,200)(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(
    x(1,T)(V)x(S)(P)xx(W)(C)(K)xx(A)xxx(V)x(1,T)
    GRMHSKGKGIASSALPYVRSPPAWCKADADSVYEQILKESKKGMSPSQIGVTLRDSHGIPQVREI</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 3858 len: 150
                                                                                                                                                                                                                                                                                                                                                 ck: 8926 len: 133
                                                                                                                                                                                                                                                                                        ck: 3575
                                                                                                               ck: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      len: 257
                                                                                                                                                                                                                                                                                               len:
                                                                                                                  len: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277
                                                                                                                                                                                                                                                                                                 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! Q00465 luffa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 P28189 schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ! P06362 marchantia polymorpha (liverwort).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! P41117 acholeplasma axanthum.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ! P73307 synechocystis sp. (strain
                                                                                                                                                                                                                                                                                                 ! Q56214 thermus aquaticus (subsp.
                                                                                                                    P26428
                                                                                                                    escherichia coli. sigma cross-react
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cylindrica (smooth loofah)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pombe (fission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30s
                                                                                                                                                                                                                                                                                                           thermophil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIXA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIXA_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAL_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSAU_SALTY
                                                                                                                                                                                                                                                                                                 SSR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRP_CHLPS
                                                                                                                      SSR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ب،</u>
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ck: 8652 len:

391

; p30872 homo sapiens

(human).

ck: 8110 len: 391

! P30873

mus

musculus

(mouse).

<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{34}(I)x(S)(V)xx(W)(C)(R)xx(I)xxx(I)x(84)
MSGENANSIGSDVTSLIQPGLEQVMODEGVQVSLINSVLGWCEVHIINPIKTSKIVQSRAFQI</pre>

ck: 3263 len: 352

! P96069 salmonella typhimurium.

ck: 9648 len:

134

! P28164 chlamydia psittaci. sulfur-rich

SECY\_RICPR ck: 3620 len: 433 ! Q9zcs5 rickettsia prowazekii.

<(x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{99}(V)x(S)(V)xx(I)(S)(H)xx(L)xx(L)x{46}
mqvfimrhgdaaldaasdsvrplftngcdesrlmanwikgqkveiervlvspflraeqtleev</pre>

<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,106)(V)xX(S)(V)xX(V)(S)(H)xx(L)xxx(I)x142}
wnifimrhgeaevmansdkarhltvygskoaflogomlkohlstlvinsldrilvspyvraoe</pre>

ck: 2974 len: 164 ! P44164 haemophilus influenzae.

ck: 7477 len: 432 ! p39444 salmonella typhimurium.

! P21625 spiroplasma melliferum.

ck: 9360 len: 161

i p76502

escherichia

phosphohistidin

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1 <\(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(91)(P)x(F)(H)xx(L)xxx(S)x(152)

MYKETYYSAFULLMHYPPPSGAGQHPQPPPLHKANQPPHGVPQLSLYEHFNSPHPTPAPADISQK
LKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYGKKKRR
SREKHQESTTETNWPRELKDGNGQESLSMSSSSSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{2}(P)x(P)(L)xx(A)(S)(R)xx(L)xxx(P)x(273)

1: MPRLSRRQLLKTAAISTALSTVPAPLLASSREKLVVPPLIEVRRGRPIVLTMQETNYPLDGSHNVT
GVDDIPLILQDMEFNNDGLQLFKQNK9HFYGNRLLVNGIEAPYLDVARGWIRLRLL
NASLARAYDLRLDNDQEMLLIAQDLGFLPKAKSVKSLVLSPGERAEILVNMMKLTTYLSLAEVNVACTKNKKYVVLRR
                                                                                                                                                                                                                                                                                                                                                                                                                          1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(148)(V)X(S)(M)XX(V)(S)(K)XX(P)XXX(T)X{114}

1: MEEKKILALIEKORIABEKIASGRKIRKRISTNATKHEREFVKVINSMFVGPATFVFVDIKGNKSHAIFGFDYGKKPGRNVDIIGOGRPIITKRGSILYLTFYGFSALNGHLENFTGKHEP
VFYVRTERSSSGRSITTVVNGVTYKNLREFIHPYNFVSSKTORIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x(188)(I)x(P)(I)x(F)(R)xx(A)xxx(G)x(187)
MFPMGTAPSPTSSPSSEGGGGGGGGGGGAADGMEEPGRNSSQNGTLSEGGGSAILISFIYS
NLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMEEPAQRWLVGFVLYTFLMGFL
LPVGAICLCYVLIIAKMRMVALKAGWQQRKRSERKITLMVMMVVMVFVICWMPFYVVQLVNVFAEQDDATVSQLSVILGYANSCANPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(1)(P)X(P)(A)XX(F)(E)X(L)XXX(C)X(258)

1: MMSDYTWFEGIPFPAFWFSKEILENSCKKFVVKEDDLIILTYPKSGTNWLIEIVCLIQTKGDPKWINFLYLYXEDMKKDTMGSIKKICDFLGKKLEPDELNLYLKYSSFQVVKENNMSNYSL
MEKELILTGFTFMRKGTTNDWKNHFTVAQAEAFDKVFQEKMAGFPPGMFPWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(43)(L)X(T)(A)XX(L)(T)(A)XX(P)X(155)

MFVLETAMAGLIVYIYYIYDEEKKRELKVRNIXMTNLLFEQFLLLTTASSLTHISAOTVPPPPPPT
KKSIELGCAORTCYEGPATLTVCFYNPPGNVIGEKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKSKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKTKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPVGAICLCYVLIIAKMRMVALKAGWQQRKRSERKITLMVMMVVMVFVICWMPFYVVQLVNVFAEQDDATVSQLSVILGYANSCANPI
TELT_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T2C1_CHVI3 ck: 7233 len: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFI_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ST14_SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSRB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSRB_CANFA
                                                                                                                                                                                                                                                                                                                                CF1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUH3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSR1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>! '</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ck: 4
                                                                                                                                                                                                                                                                                                                                ck: 5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ck: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ck: 5285 len: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x{82}(I)x(P)(A)xx(V)(S)(H)xx(V)xxx(L)x{85}
mrllsevvlalfavtqaeegarllasksllnryavegrdltlqyntynvgssaaldvelsddsfpf</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ck: 8093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x{82}(I)x(P)(A)xx(V)(S)(H)xx(V)xxx(L)x{85}
MRLLASVLLALFAVSHAEEGARLLASKSLLNRYAVEGRDLTLQYNIYNVGSSAALDVELSDDSFPF</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ck: 8392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ck: 9240
                                       3375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     len: 285
                                                                                                                                                                                                                                                                                                                                len: 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  len: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          len: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               len: 391
                                           len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          len: 311
                                   167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! P52283 chlorella virus il-3a (cv-il3a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! P50235 rattus norvegicus (rat). alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! P44847 haemophilus influenzae. sufi protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! P43308 homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                ! P36402 homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Q41495 solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! P28646 rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ! P23438 canis familiaris (dog). translocon
                                   015273 homo
                                       sapiens
                                       (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (potato). sts14
                                       telethonin
                                                                                                    GGGGGGGAGCPQQQQAQQQSPRRVAVPVLVKDGKPCQAGAPAPGAGSLQGHAQQQAQQAQAQAAQAAAAA1SVGSGGPGLGAHPG
```

ц	<b>!</b>	$ \begin{array}{l} <\langle X\rangle\{1,200\}\{L,I,V,M,A,P\rangle X(P,T,S)\{L,I,V,M,A,P\rangle X(L,I,V,M,A,F,Y,W,X,139\}\{L\}X(P)\{V\} xx(V)\{S\}\{X,xx(A)xxx(S)x\{12\}\\ & \text{MATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLHEEDTQRHETYHQQGQCQVLVQR} \end{array} $
	TELT_MOUSE	ck: 5613 len: 167 ! O70548 mus musculus (mouse). telethonin
щ	1:	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T.S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{139}(L)x(P)(V)xx(V)(S)(K)xx(P)xxx(T)x{12} matselscovseenoerreafwaewkdltlstrpeeggslheedtorhetyhrogocoavvor</pre>
<b>-</b>	TRAM_AGRT6	, t
٣	1:	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{13}(L)x(P)(L)xx(L)(T)(R)xx(P)xxx(L)x{73} meledanytkkvelrpligltrglpptdletitidairthrrlvekadelfqalpetyktg</pre>
	TRMD_SYNY3	ck: 6210 len: 231 ! P72828 synechocystis sp. (strain pcc 680
1 YTRPPVFR	1: PPVFRGLAVPPVLLSGNH	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(70)(V)x(S)(L)xx(L)(S)(K)xx(V)xxx(T)x{145} MQFDVLTLFPDFFTSPLQSGLLGKALEKAIASVNLINPRDFTTDKHRRVDDEPYGGGVGMVIK GNHQAIAQWRLEQQEETTQQRRPDLWQKWQDRQPSP</pre>
	TRMU_SCHPO	ck: 7997 len: 415 ! Ol3947 schizosaccharomyces pombe (fissio
1 PIDKRKDQ CFVSPNVG	1: TLFLCTIRKEALE RKFRKFLQRYLNF	<pre>&lt;(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{200}(L)x(P)(L)xx(W)(T)(K)xx(Y)xxx(A)x(199) 1:</pre>
	TRMU_YEAST	ck: 8415 len: 417 ! Q12093 saccharomyces cerevisiae (baker's
1 PKDQSYYLSQ SQHGKFKNFI	1: SQINSTVLSSLLL FLKHYLPSSPGDI	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{196}(L)x(P)(I)xx(L)(T)(K)xx(Y)xxx(A)x(205) 1:</pre>
	TRNH_DATST	ck: 5293 len: 268   P50165 datura stramonium (jimsonweed) (c
1 TKSLACEWAKD SEVSSLVTYLC	1: AKDSIRVNAVAPW YLCLPTASYITGQ	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,X,W x{162}(L)x(S)(I)xx(A)(S)(K)xx(I)xxx(T)x{90}  1:</pre>
	TRPF_CRYNE	ck: 2342 len: 312   P27710 cryptococcus neoformans (filobasi
1 GLDLVQLH SGGGGEGK	1: GDEPQAWAKFIPV AFPWEHAKRLIQS	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W</pre>
	TTF1_CANFA	ck: 4988 len: 371 ! P43698 canis familiaris (dog). thyrold t
<b>.</b>	- <b>-</b> -	$<(x)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y$
RRFKQQKY	LSAPEREHLASMI	HLTPTQVKIWFQNHRYKMKRQAKDKAAQQQLQQDS

VE2_HPV03 ck: 4819 len: 383 i p36778 human papillomavirus type 3. regulad (X){1,200}(L,I,V,M,A,P)X(D,I,I,V,M,A,P)X(L,I,V,M,A,F,Y,W)(C (X){1,200}(L,I,V,M,A,P)X(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W)(C (X){1,200}(L,I,V,M,A,P)X(I)X(310) (X){1,200}(L,I,V,K)XXX(I)X(310) (X){1,200}(L,I,V,K)XXX(I)X(310) (X){1,200}(L,I,V,K)XXX(I)X(310) (X){1,200}(L,I,V,K)XX(I)X(310) (X){1,200}(L,I,V,K)XX(I)X(I)X(I)X(I)X(I)X(I)X(I)X(I)X(I)X(	VANS_ENTEC ck: 3601 len: 384 i Q06240 enterococcus faecium (streptococcus coccus coccu	USO2_HSVEK ck: 5996 len: 303 ! p32517 equine herpesvirus type 1 (strain ke (x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) (x)[2,5]	UMUD_ECOLI ck: 8403 len: 139 ! P04153 escherichia coli. umud protein (ec 3  <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)  x{73}(V)x(S)(A)xx(A)(S)(H)xx(I)xxx(A)x[50]  1: MLFIKPADLREIVTEPLFSDLVQCGFPSPAADTVEQRIDLNQLLIQHPSATYFVKASGDSMIDGGI	UBC7_DROME ck: 1891 len: 153 ! p52487 drosophila melanogaster (fruit fly).  <(x)[1,200](L,I,V,M,A,P)X(P,T.S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x([36](M)X(T)(A)XX(F)(T)(K)XX(A)XXX(P)X MAATRRLTRELSDLYEAKMSTLRNIESSDESLLMWTGLLVPEKAPYNKGAXRIEINEPPQYPEMPF  1: MAATRRLTRELSDLYEAKMSTLRNIESSDESLLMWTGLLVPEKAPYNKGAXRIEINEPPQYPEMPF	TXF8_DENAN ck: 8703 len: 81 ! P01404 dendroaspis angusticeps (eastern gre  (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)  x(18}(A)x(T)(M)xx(Y)(S)(H)xx(P)xxx(A)x(47)  x(18)(A)x(T)(LLTLLYTIVCLDLASTMICYSHKTPQPSATITCEEKTCYKKSVRKLPAIVAGRGCGCPS  1: MKTLLLTLLYTIVCLDLASTMICYSHKTPQPSATITCEEKTCYKKSVRKLPAIVAGRGCGCPS	. ENYFOIG ,M,A,F,Y,W )QHAVGHHGA )SGGAGLGAHE	se). thyroid tra (L,I,V,M,A,F,Y,V PPAAAMQQHAVGHHGA AAISVGSGGAGLGAHI	<b>р</b> ж
(1, I, V, M, A, P)X(P, T, S)(L, I (57)(V)x(P)(P)xx(V)(S)(K)xx(A)xxx (57)(V)x(P)(P)xx(V)(S)(K)xx(A)xxx TPARLMAYQEKTLDLYEADSNDLNAQIEHWKLT EVERTETAVHLOTETSKYSAVSYGKOTHLQ QOSVDSTIRGLYTATECTNKGRVAHTTCTAPII	1: VITCPE DSSTIS	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,M x(63)(Y)x(P)(P)xx(I)(S)(K)xx(A)xxx(I)x(289) 1: MKMQTFKESLSENLSALQDKILDYENDSKDINGOISYWQLIRLENAILFTAREHGITKLNHQ FKSECEKYGNSNTWEVQYGGNVIDCNBSMCSTSDITVROLOHASTSTPKI ASVGTPKPHIQTPATKRPRQCGLTEQHHGRVNTHVHNPLLCSSTSNNKRRKVCSGNTTPIIHLKGDKNSLKCLRYRLRKYADHYS, ASVGTPKPHIQTPATKRPRQCGLTEQHHGRVNTHVHNPLLCSSTSNNKRRKVCSGNTTPIIHLKGDKNSLKCLRYRLRKYADHYS, ASVGTPKPHIQTPATKRPRQCGLTEQHHGRVNTHVHNPLLCSSTSNNKRRKVCSGNTTPIIHLKGDKNSLKCLRYRLRKYADHYS, ASVGTPKPHIQTPATKRPRQCGLTEQHHGRVNTHVHNPLLCSSTSNNKRRKVCSGNTTPIIHLKGDKNSLKCLRYRLRKYADHYS, ASVGTPKPHIQTPATKRPRQCGLTEQHHGRVNTHVHNPLLCSSTSNNKRRKVCSGNTTPIIHLKGDKNSLKCLRYRLRKYADHYS, ASVGTPKPHIQTPATKRPRQCGLTEQHHGRVNTHVHNPLLCSSTSNNKRRKVCSGNTTPIIHLKGDKNSLKCLRYRLRKYADHYS, ASVGTPKPHIQTPATKRPRQCGLTEQHHGRVNTHVHNPLLCSSTSNNKRRKVCSGNTTPIIHLKGDKNSLKCLRYRLRKYADHYS, ASVGTPKPHIQTPATKRPRQCGLTEQHHGRVNTHVHNPLLCSSTSNNKRRKVCSGNTTPIIHLKGDKNSLKCLRYRLRKYADHYS, ASVGTPKPHIQTPATKRPRQCGNTHRANGANGANGANGANGANGANGANGANGANGANGANGANGA	x(57)(V)x(P)(A)xx(V)xx(A)xxx(A)xx(A)xx(A)xx(A)xx(A)	LTYGVTGTWEVHVAGTVIHHTSASYSSTQASASDDEFLSPIRTAVSPVEAFVAASA ESTGAGRAAPPTQALCSAQAPTSPPAKRQRVIVGQOHPRPDSTRTVGEGEVECYNKRSISDSNRTDPRWGHGDTDSVPVIHLRGD VE2_HPV31 ck: 9656 len: 372 ! p17383 human papillomavirus type 31. reg VE2_HPV31 ck: 9656 len: 372 ! p17383 human papillomavirus type 31. reg	VE2_HPV2A ck: 734 len: 391 ! p25482 human papillomavirus type 2a. reg  (x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W  x(57){A)Xx(P)(A)Xx(V)(S)(K)XX(A)XXX(I)X(318)  METLANRLDACOETULELYEKDSNKLEDQIKHWAQVRLENVMLFKARECGMTRVGCTAVPALT  1: METLANRLDACOETULELYEKDSNKLEDQIKHWAQVRLENVMLFKARECGMTRVGCTAVPALT	VE2_HPV28 ck: 1816 len: 376 ! p50771 human papillomavirus type 28. reg  (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W  x{57}(V)x(P)(P)xx(V)(T)(K)xx(A)xxx(I)x{303}  x57}(V)x(P)(F)xx(V)(T)(X)xx(A)xxx(I)x(A)XxX(I)xYX(I)XYX(I)XYX(I)XYX(I)XYX(I)XYX(I)XYXX(I)XYXX(I)XYXX(I)XYXX(I)XYXX(I)XYXXX(I)XYXXXXXXXXXX	VEZ_HPV18 ck: 5006 len: 365 ! P06790 human papillomavirus type 18. reg  <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W  x(61)(Y)x(P)(A)xx(I)(S)(K)xx(A)xxx(I)x(288)  MOTPRETISERISCYODIXIIDHYENDSKUIDSQLQIWQLIRWENAIFFAAREHGIQTLINHQVV  SECEKYGNTGTWEVHFGNNVIDCNBMCSTSDDTVSATQLVKQLQHTPSFYXSTVS  VGTAKTYGQTSAATRPGHCGLAEKQHCGFYNPLLGAATPTGNNKRRKLCSGNTTPIIHLKGDRNSLKCLRYRLRKHSDHYRDISS	VE2_HPV10 ck: 273 len: 376 i p36781 human papillomavirus type 10. reg  <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W  x[57](Y)x(P)(P)xx(V)(T)(K)xx(A)xxx(I)x[303]  METLANKLDACOOKMLELYEKDSDKLEDOITHWHLLRVENALLYKARECGLTHIGHQVVPPLS  CVYGETGKWEVHYGGKVIHHDAFDPVSSTREISTPGPVCTSNTTPASTOAQVGASE  CVYGETGKWEVHYGGKYCHGKAAERAGGGYDSDRTRLCDTRSAHPVRHPSDPDCAPVIHLRGDPNSLKCFRYRLHHG

1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{125}(L)x(S)(I)xx(V)(S)(R)xx(I)xxx(S)x(6)  1: MSQGSRPTSSDIAVNQRECVKVEGFKVVSTRLRSAEYESFSHQARLLGLSDSMAIRVAVRRIGGFU	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X,(25)(L)x(S)(I)xx(V)(S)(R)xx(I)xxx(S)x(6)  1: MSQGSKPTSSDIAINQRVGATVEGFRVVSTRLRSAEYESFSHQARLLGLSDSMAIRVAVRRIGGFL  VID1_AGRT5 ck: 2312 len: 147   P18591 agrobacterium tumefaciens. t-dna bor	1	VIB8_AGRT6 ck: 2646 len: 230 i p09781 agrobacterium tumefaciens. virb8 prc  (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(G) (X){2}{A}X(S)(A)XX(L)(S)(X)XX(A)XX(X)X(Y) (X){2}{A}XX(L)(S)(X)XX(A)XXX(A)X(Y) (X){2}{A}XX(A)X(Y) (X){2}{A}XX(A)X(Y) (X){2}{A}XX(A)X(A)X(A)X(A)X(A)X(A)X(A)X(A)X(A)X(A	VIB8_AGRT5 ck: 5994 len: 237 ! P17798 agrobacterium tumefaciens. virb8 prd  <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C  x{29}(A)xX(L)(S)(K)xX(A)xxx(T)x{192}  MGGEYALLVARETLAEHYKEVEAFOTARAKSARRLSKVIAAVATIAVLGNVAQAFTIATMVPLIH  krtlivDgkmpmastwtatvryekvislpgrlrlinpgglvvtsyQTsedtvsnag  HSEP	VGLM_HSVSA ck: 7071 len: 366 ! Q01017 herpesvirus saimiri (strain 11). gly  <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C	VGLI_HSV2H ck: 501 len: 372 ! p13291 herpes simplex virus (type 2 / strai  <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q	ESVYPEECZAELPYAQVKAVADLYALCWOSGEVYTYTPOPEKATIWINNYSGTCYQ  EYVKLERLOEALAGNSPVIPGGWISCSERWPDNDESKPIAIFTGKCLGOGMFVATYDDDGFFDYWEGMEIIGVSHWMQLPDPPL  VGG_BPG4 ck: 4484 len: 177 ! p03644 bacteriophage g4. major spike protei  VGG_BPG4 ck: 4484 len: 177 ! p03644 bacteriophage g4. major spike protei  (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)  X{29}(V)XX(E)(S)(V)XX(L)(S)(R)XX(I)XXX(A)X{132}  1: wfQKFISKHNAPINSTQLAATKTPAVAAPVLSVPNLSRSTILINATTTAVTTHSGLCHVVRIDETN	VEAA_BPP22 ck: 7758 len: 317 ! Q03544 bacteriophage p22. eaa protein. 10/1  <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
VRPR_SALDU	VP8_BPPH6 1 1:	VMEM_PVMR 1	1 1: VMEM_LVX 1	1 DIGVNEQNE 1:		VMA2_BRSVA 1 DINVDEQNE	1: VLF1_NPVOP  1 DSKIKLMNSDYVHDRGLIRG DTIGLKRKRSRKNTLNNIKT	VID1_AGRT6
ck: 7061 len: 297 ! P24417 salmonella dublin. vir <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,	<pre>ck: 6252 len: 149 ! P07579 bacteriophage phi-6. major nucl &lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y x(18)(A)X(T)(P)XX(V)(S)(R)XX(A)XXX(S)X(115) MLLPVVARAAVPAIESAIAATPGLVSRIAAAIGSKVSPSAILAAVKSNPVVAGLTLAQIGS</pre>	<pre>ck: 3415 len: 109</pre>	<pre>&lt;(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F)XX(L)(S)(R)XX(L)XXX(G)X(68) x{22}(V)Xx(S)(I)XX(I)(S)(R)XX(L)XXX(G)X(68) xx(2)(V)X(S)(I)XXX(I)XXX(I)XXX(G)XX(I)XIIIIIIIIIIII</pre>	CK: 5059 Len: 100 (Q84132 OVINE RESPIRACOTY SYNCYTHA (X)[1,200](L,I,V,M,A,P)X(F,T,S)(L,I,V,M,A,P)X(L,I,V,M,X)(R)](T)(K)XX(A)XXX(M)X[87](X)XX(L,I,V,M,X)(R)X(R)X(R)X(R)X(R)X(R)X(R)X(R)X(R)X(R	ck: 9828 len: 194 ! P04545 human respiratory <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX( x(83](I)x(S)(I)xx(I)(T)(K)xx(A)xxx(M)x(95) MSRRNPCKFEIRGHCLNGKRCHFSHNYFEWPPHALLVRQNFMLNRILK	<pre>\ ck: 6337 len: 186   P29792 bovine respiratory syncytial &lt;(X){1,200}{L,I,V,M,A,P}X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,P) x(83}(L)x(S)(I)xx(I)(T)(K)xx(A)xxx(M)x(87) MSRRNPCKYEIRGHCLNGKKCHFSHNYFEWPPHALLVRQNFMLNKILKSMDRNNDTLS)</pre>	X A	<pre>ck: 4145 len: 147 '! P06667 agrobacterium tume &lt;(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX( x{125}(L)x(S)(I)xx(Y)(S)(R)xx(I)xxx(S)x(6)</pre>

x(23](A)x(S)(V)xx(I)(T)(R)xxx(I)x(258)

MDFLINKKLKIFITIMETGSFSIATSVLYITETPLSRVISGLERELKQRLFIRKNGTLIPTEFAQT
GKPDINRLAGTPVLFHEGAKNFNLDTIYHEFEQTLGITNPAFSFDNVDLFSSTYRL
QQGLANLLIPVRVCRALGLSTDHALHIKGVALCTSLYYPTKKRETPDYRKAIKLIQQELKQSTF

VRPR\_SALTY

ck: 7032 len:

297

! P13041 salmonella typhimurium.

hypothetic

Y209\_MYCGE

ck:

308

P47451

mycoplasma

MHYVHVHRVTTQPRNKPQTKCPSGGQSQGPRGQFLDTVLAAMCPIAMLLTADPGMPPTCLWHT

WN11\_CHICK

WN11\_COTJA

WN11\_HUMAN

WN11\_MOUSE

WNT4\_DROME

Y021\_NPVOP

YO40\_HUMAN

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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(23)(A)X(S)(V)XX(I)(R)XX(I)XX(I)X(258) (D)XX(I)X(258) (D)XX(I)X(1)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)XIX(I)X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 

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x(115)(A)X(S)(A)XX(I)(S)(H)XX(A)XXX(I)X(223)
x(115)(A)X(S)(A)XX(I)(S)(H)XX(A)XXX(I)X(223)
mrakpoyccallealotgoycygikulaknepsalalnotohckolegluvsaqvolcrsulela
vkktgsoanklmrlhusevgroalasleakokchovsgscsirtomkgloelopv
aadlkttrylsatkvvhrpmgtrkhlvpkdldirpvkdwelvylosspdfcmknekvgshgtodrocnktsngsdscdlmccgrgxnpy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 

<
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 < \langle (x) \{1,200\} (L,I,V,M,A,P)X(P,I,S) (L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) (C,I,V,M,A,F,Y,M,I) (C,I,V,M,A,F,X,M,I) (C,I,V,M,A,F,Y,M,I) (C,I,V,M,A,F,X,M,I) (C,I,V,M,I) (C,I,V
                                                                                                                                                                                                                                                           1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Z,Y,W)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M)(Z,Y,M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 4030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ck: 3073 len: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ck: 1689 len: 354 ! P48615 mus musculus (mouse). wnt-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ck: 8394 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 562
<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d
x(119)(L)x(T)(V)xx(M)(S)(H)xx(A)xxx(S)x{18}
                                                                                                                                                 4815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       len: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! P49339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! 096014 homo sapiens (human). wnt-11 protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! P51891 coturnix coturnix japonica (japanes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! P40589 drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i 010280 orgyia pseudotsugata
                                                                                                                                                      Q15053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gallus gallus (chicken).
                                                                                                                                                                 omo
                                                                                                                                                      sapiens (human). hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multicapsid po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wnt-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y280_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y209_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y425_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7373_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y464_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y464_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 9511 len: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 6533 len: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 4876 len: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 2944 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 2836 len: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 5866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p47522 mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 083388 treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i p75172 mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p47702 mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P75485 mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p75112 mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genitalium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae. hypothetic
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YCJ	<pre>&lt;(x){1,200}(L,1,v,m,a,p)x(P,T,S)(L,1,v,m,a,P)xx(L,1,v,m,a,F,y,m)(Q x{8}(P)x(T)(L)xx(M)(S)(K)xx(V)x{192} 1:</pre>
DPLACIEDPRHSE ISSDEASEKYLFA	YABP_ECOLI ck: 98 len: 216 ! P39220 escherichia coli. hypothetical 24.8
1	<pre>((X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x[98](P)X(S)(A)XX(A)(S)(R)XX(A)XXX(I)X{8} 1:</pre>
AC-1	YA32_PSEAE ck: 6657 len: 122 ! P21485 pseudomonas aeruginosa. hypothetical
1 YCG	<pre>-(X)[1,200](L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F,Y,W)(C) x{47}(A)x(S)(V)xx)(S)(R)xxx(G)xxx(G)x(266) MELLEYLKROBEVLFLCHHUNDPDAYGSCVALKYLASQLNPNGKFRISADSVSKLSRNILNEIGERY KDISFQKILYLLSQESDVSKRTAHLKACSRMEIREFDKLRIALSHVSSHEASCAKT IVSIGADVAFVVAVRKKEKEIRVSARCRKHVSKYVHLGNLMEKIGKELGGSGGGHSEAGGLNAPYDKSKSKEKVIKEVLNLCYKRFVE IVSIGADVAFVVAVRKKEKEIRVSARCRKHVSKYVHLGNLMEKIGKELGGSGGGHSEAGGLNAPYDKSKSKEKVIKEVLNLCYKRFVE</pre>
AANIH	y988_метла ck: 9981 len: 329 ! Q58395 methanococcus jannaschii. hypothetiq
1 УСВ	<pre>(X){1,200}{L,I,Y,M,A,PX(P,T,S)(L,I,Y,M,A,P)X(P,T,Y,M)(Q)</pre>
VIMLSLALSFILP YAIEGIRYIYSNT	r953_MYCTU ck: 883 len: 282   P71557 mycobacterium tuberculosis. hypothet
<b>ус</b> з	<pre>((x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(19)(I)x(S)(I)xx(I)(T)x(X)xx(L)xxx(L)x(135) 1: MKGINPFYFYIGMALILASIVSILLITKSILLFILLAFGSLVGITLILIXISRKILKIDKGRLKKE</pre>
YETIGVTIDVSIL	Y79B_METJA ck: 2865 len: 170 ! P81233 methanococcus jannaschii. hypothetic
1 YC2	<pre>(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(164)(1)x(P)(L)xx(V)(S)(R)xx(L)x(260) 1:</pre>
	Y788_BORBU ck: 1619 len: 440 ! O51728 borrelia burgdorferi (lyme disease s
1 YVGISNYIKDKHI	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{84}(I)x(S)(I)xx(Y)(S)(H)xx(I)xxx(L)x(2)  1: mvgnmnirdkiksiknwinfikpiitivgivisavaftisilmgmlflilflilitifsktirki
¥C0	ү70A_METJA ck: 4119 len: 102 ! P81311 methanococcus jannaschii. hypothetic
RLAISMGIKTIME IADYKAAQKLKSA	**(A)[1,200](H,1)(H,1)(H,1)(H,1)(H,1)(H,1)(H,1)(H,1)
твг	Y503_METJA ck: 6767 len: 406 ! Q57926 methanococcus jannaschil. putative 2
1 VTNDLSLVISEFS	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x{135}(L)x(P)(A)xx(F)(T)(H)xx(L)xxX(I)x{80} 1:</pre>
<b>УВС</b>	Y4TG_RHISN ck: 6923 len: 231   P55661 rhizobium sp. (strain ngr234). proba

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YIS.
                                                                                                                JI_ECOLI ck: 6021 len: 262
                                                                                                                                                                                                                                              GZ_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                            BQ_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                 38_PORPU ck: 4681 len: 291 ! P51321 porphyra purpurea. hypothetical 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21_METJA ck: 2920 len: 299 ! Q58618 methanococcus jannaschii. hypothe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08_KLEPN ck: 4280 len: 373 ! Q48454 klebsiella pneumoniae. hypothetic
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                                                                                                                                                                      ۲.
                                                                                                                                                                                                                                                                                                                      H
                                                                                                                                                                                                                                                                                                                    <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x[44](A)x(T)(L)xx(A)(T)(K)xx(V)xxx(P)x{122}
MITMKKSVLTAFITVVCATSSVMAADDNAITDGSVTFNGKVIAPACTLVAATKDSVVTLPDVS</pre>
                                                                                                                                                                                                                                                                                                                                                                                            ck: 3224 len: 182 ! P75855 escherichia coli. hypothetical fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 3388 len: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{142}(Y)x(T)(L)xx(L)(T)(K)xx(M)xxx(I)x{34}
MDLLFDEFRAAHVPVEEMATHYIPEAARQIGAAWDSDRIGFAQVTIAISRLQELLHALQTLVT</pre>
                                                                                                                                                                    <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{7}(L)x(S)(A)xx(I)(T)(R)xx(A)xxx(L)x{55}
MHQNSVTLDSAGAITRYFAKANLHTQQETLGEIVTEILKDGRNLSRKSLCAKLLCRLEHAT</pre>
                                                                                                                                                                                                                                              ck: 1943 len: 78
                                                                                                                  ! P51983 escherichia coli. hypothetical 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! 031458 bacillus subtilis. hypothetical 2
                                                                                                                                                                                                                                              ! P75991 escherichia coli. hypothetical 8.
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JZ\_ECOLI

ck: 51

len: 299

 $<(x)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,F,Y,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,W,F,Y,$ 

! P77333 escherichia coli. hypothetical tr

x(167)(L)xx(F)(C)(K)xx(F)xx(L)x(L3) x(167)(L)xx(S)(L)xx(F)(C)(K)xxx(L)x(L3) MLCGLTDVILPGKDAITTQIIDFDKNIGFNVEETESALTLTLKGATWGANSFDAKLEFQCNDN	1: VVSRILGRSTAQRGGYSAV	<pre>&lt;(X) [1,200] (L,I,Y,M,A,P)X(P,T,S) (L,I,Y,M,A, &lt;(X) [1,200] (L,I,Y,M,A,P)X(P,T,S) (L,I,Y,M,A, x(27) (P)X(P) (Y)xx(A)(T) (R)xx(Y)xxx(I)x(23 MAKVTRDDVARLAGTSTAVVSYVINNGPREVAPATRERVLA MAKVTRDDVARLAGTSTAVVSYVINNGPREVAPATRERVLA</pre>
ck: 8234 len		o ck: 9954 len: 66   Q05954 streptomyces coelicolor. hypothetica
EALGPVMSQHTG	1:	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(34)(I)x(S)(L)xx(Y)(C)(R)xx(L)xxx(S)x{57} maaqnpladiqvykrykakrrmegqkknsctiayidslqyycrrslshkscfpfpsqhafsrpi</pre>
<pre></pre> <pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T, &lt;(X){1,200}(L,I,V,M,A,P)X(P,T, </pre>	1	r ck: 6897 len: 107 ! P53138 saccharomyces cerevisiae (baker's ye
MLIMHQVVCATTNE	1:	<pre>&lt;(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)An(L,1,Y,M,A,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y</pre>
<(X){1,200}(L,1 x{144}(V)x(T)	н	ck: 7782 len: 148 ! P31653 bacteriophage sp01. hypothetical 16.
VVVCDRPAPRILELAQTAQLVVVGSHGRGGFPGMHLGSVSRAVVNSGQAPVIVARIPQDPAVPA ck: 3873 len: 173   p39411 escherichia coli. hypothetical 18	MLARRISGWQDRYPDVVVHK	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x{7}(A)x(S)(P)xx(M)(S)(R)xx(A)xxx(M)x(125) MPLSGEYAPSPLDWSREQADTYMKSGGTEGTQLQGKPVILLTTVGAKTGKLRKTPLMRVEHDGQYA</pre>
<pre>&lt;(X){1,200}(L,1,V,M,A,P)A(F), 5)(L,1,Y,M,F); &lt;(X){1}(1)(Y)(X)(T)(L)(X,Y)(T)(T)(T)(T)(T)(T)(T)(T)(T)(T)(T)(T)(T)</pre>	;	ck: 497 len: 148 ! Q10772 mycobacterium tuberculosis. hypothet
ck: 1836 len: 317   Q10862 mycobacterium tuberculosis. hypot	VIDAM 96.7X	<pre>&lt;(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x(49)(L)x(P)(P)xx(F)(T)(K)xx(M)xxx(S)x(63) MEELICTYPYHSNLFMFLFLFECPSKRARRGHPKFLFTLCYKSNHLIPKLLPPSLFTKRVMLNPSS</pre>
<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,F)XA(L,I,V,M,A,F)XA(L,I,V,M,A,F),XX(I)X{9}\ x{49}(V)x(P)(P)xx(L)(T)(H)xx(I)xxx(I)x{9}\ MGEVRVVGIRVEQPONQPVLLLREANGDRYLPIWIGQSEAAAIALEQQGVEPPRPLTHDLIRD</pre>	1	ck: 5798 len: 128   P40057 saccharomyces cerevisiae (baker/
ck: 7074 len: 164   Q50604 mycobacterium tuberculosis. hypot	YIZ9_MYCTU	MNSNEIENFIYLNNTLLSEVPEPNSVFYFKKESNSKLFHGSLULEFSSRCGLERRAFFLOGGRKDVS SLVPNIMPHYPDEVTAKSAPKDDFYVPRETRKHGIS TSAYWYHNEVHGIHSKGRFYOPPIEFRTVRLRKTRNAIGVPNKKYMIEGKCHQCNKWIRCQGRKDVS
x{{20}{(1)x(T)(1)xx(L)(5)(1)xx(L)(x(L)(x)(x)(x)(x)(x(L)(xx(L)(xx(L)(x)(x)(x)(x(L)(x)(x)(x)(x)(x(L)(x)(x)(x)(x)(x)(x)(x)(x)(x)(x)(x)(x)(x)	1: ILVMMATQMFLDGIRMWMKG	T
٢		The section of the se
ck: 1678 len: 197   P46851 escherichia coli. hypothetical 21	YHGN_ECOLI	A(X) L, 200 (L), L, V, E,
MANNYMKLIATTÄÄLISVYSTULAKSVMALKADOOMANIN TUURENSSAGVAKKENEVKIRKEY SSMGVAUTKSDETRVSINDISMTEEDBISKOVRKKLA RDDILSPIDCEHRAINAVRDEALRHLPELGTMPGIFGLSIATWILTKVSGYPMKENEVKNRLKFY	1; NLESKYDLLEYAHHNKIDVISSMGVALKSDPTRVSINI KRGIATGISVVFSNEMLDPRRDDILSPIDCEHRAINA	ck: 8869 len: 174   Ol4185 schizosaccharomyces pombe (fission y
(M) xx(A) (T) (K) x	1 1100 _ 1 1100 _ 1 1100 _ 1	x(1)[1,20](1,1); x(1)[1,x(T)[1,x](T)[K)xx(L)xxx(S)x(100) x(15)(L)x(T)[1,x](T)[K](K)xx(L)xxx(S)x(100) psaraykdrmesboletlekitkyilkllsktylevenievihhekakhliiemidyiepsivv
Av. 5560 len. 429 i P38756 saccharomyces cerevisiae (baker's	TGHPLTGUS.	ck: 6054 len: 131   p87132 schizosaccharomyces pombe (fission y
<(X) {1,200} {L, I, V, M, A, P}X(P, T, S) {L, I, V, M, A, P}XA(U, I, V, P, A, V,	1: LRIKKGIINPPIGRDRSHPIR	MKTITSDEDETITRVDTICTIAKLPYLLNPRLKEPWGHFFKTYMDGYHKYKINGTKSDETDES TGSDRYKILGEILDKIDSGCNKEGNSCSYWYIGDS PROSKFIKITEKIIGIPKDKISSFEADNGPAWLQFCEKEGGKGAYLVKSWDSLKDLIMQVTKM
ck: 1929 len: 302 ! p54604 bacillus subtilis. hypothetical 3	YHCT_BACSU	<pre>(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X){1,200}(L,I,V,M,A,F,Y,W)(C,X)</pre>
SHOSE LIENSWYDD Y IN Y Y FRANK GETRATGRDPTIVFRWQGWYGHHQHPGCSCGYGVEERQFRP AABFAPGSALRVEPVTPQVTRRKGSTRATGRDPTIVFRWQGWYGHHQHPGCSCGYGVEERQFRP	TTGWCVRVADYLRLLQWVGKK AILGLAEKDPLARIGGRLNPL	ck: 1969 len: 317 ! P25616 saccharomyces cerevisiae (baker's ye
1 <(x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) xx(f)x(f)(L)x(T)(P)xx(V)(C)(K)xx(V)xxx(L)x(241)	1	x(168)(V)x(5)(P)xx(F)(S)(R)xx(V)xxx(V)x(14-7) MKREEIADLMAFVVVAEERSETRAAARLSMAGSALSQIVRRIEERLGLRLLTRTTRSVVPTEAGEH TSGTANRWRLIRGGREVEVRMEGQLLLNTIDLIID EKKLIRVLDKFTPDLPGYHLYYPHRRHAGSAFSLFIDRLKYKGAV
ck: 3269 len: 319 ! P10941 cryphonectria parasitica (chesnut	YHA1_CRYPA	

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YF58\_MYCTU

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YG29\_BPSP1

YGK9\_YEAST

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YGLR\_STRCO

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x{168}(V)x(S)(P)xx(F)(S)(R)xx(V)xxx(V)x{115}
MKREEIADIMAFVVVAEERSFTRAAARLSMAQSALSQIVRRIEERLGLRLLTRTTRSVVPI
RSVPTSVSQLIDHQAINLYLPTSGTANRWRLIRGGREVRVRMEQULLNTIDLIID
AAIDGHGLAYLPYDQVERAIKEKKLIRVLDKFTPDLPGYHLYYPHRRHAGSAFSLFIDRLKYKGAV
                                                                                                                                                                              1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F)XX(L,I,V,M,A,F)XX(L,I,V,M,A,F)XX(L)XXX(G)X{282}
x146)(P)X(S)(A)XX(L)(S)(K)XXX(G)X{282}
MNSNEIENFIYLUNTILESVPEPNSYTPRGETSSSKLPHQSDLEEPSSACSLSKNTIID
VLENHITSREPHEYTKLDDVSLVPNNNEHYPDEDVTAKSAPKDDFYVPRETROHGIS
VLENHITSREPHEYTKLDDVSLVPNNNEHYHÖIHSKGRPYQPPIEFRTVRLRKTRNAIGVPNKKYMIEGKCHQCNKWIRCQ
KLGLCPICSHQGEFIWLRTKTSAYWYHMNEVHGIHSKGRPYQPPIEFRTVRLRKTRNAIGVPNKKYMIEGKCHQCNKWIRCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCQ5_YEAST ck: 1969 len: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDM1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDSA_SCHPO
                                                                                                       YER4_YEAST ck: 5798 len: 128
                                                                                                                                                                                                                                                                                                                                                               YDTG_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ck: 8869 len: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F)
x{15}(L)x(T)(L)xx(I)(T)(K)xx(L)xxx(5)x{100}
DPSARAVKDRMESEQLETLEKITKYILKLLSKTVLEVEVNIEVIHHEKAKHLIIEMIDYI</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ck: 6054
                                                                                                                                                                                                                                                                                                                                                               ck: 3748 len: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                         <(x){1,200}{L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F)
x{97}(L)x(S)(I)xx(F)(S)(R)xx(A)xxx(P)x{61}
mTSQLEKEAREWIEETLHTKLNAQLDLLDQLQSGVILCRICKEALGANIRYKESNMPFVQ</pre>
<(X){1,200}{L,I,V,M,A,P}X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F)
x{49}(L)x(P)(P)xx(F)(T)(K)xx(M)xxx(S)x{63}
MEELICTYPYHSNLFMFLFLFFCPSKRARRGHPKFLFTLCYKSNHLIPKLLPPSLFTKR</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        len: 131
                                                                                                                1 P40057 saccharomyces cerevisiae (bake
                                                                                                                                                                                                                                                                                                                                                                      ! 014220 schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! P25616 saccharomyces cerevisiae (bake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ! P87132 schizosaccharomyces pombe (fis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 014185 schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                            pombe (fis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pombe (fis
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ı	1: IRVSALTPSTVASDMS WSTNP	۲	1 GQLIGDEGI	1 HEKGLEKFY TEQRAKFML	1 GAGEFEPFS VHRIPISKP	н	н	H	P
YPDC_ECOLI	1: TVASDMSIELNL	YOTC_CAEEL 1:	YORL_TTV1 1: HFIEAKKLISNR	YNU6_CAEEL  1: EAVSTAFMRHVN THSSSGFKHALK	1: KLSARQDARKTY KCPDHLQKILQM	1:	1:	YM27_MARPO  1:  YN06_YEAST	YKFF_ECOLI
ck: 4986 len: 285   P77396 escherichia coli. hypothetical trans <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d	100) (L.I.V.M.A.P.)X(P.T.S) (L.I.V. 100) (L.I.V.M.A.P.)X(P.T.S) (L.I.V. (V)x(S) (A)xx(A)(S) (K)xx(Y)xxx(T ALITGGGRGIGRATALALAKEGVNIGLIGRI DPEDLAEYMVAOLKLDPRIFIKTAGL	9212 len: 161   Q10120 caenorhabditis elegans. hypothet ){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y, {88}(A)x(T)(V)xx(M)(S)(H)xx(A)xxx(A)x(57) PLGFIGYEFGDDEMFVQQMIEKKSNAEQAKMLEQQKKMLECTETMPEESEPVPMKCLDF	YORL_TTV1 ck: 9154 len: 232 ! p19296 thermoproteus tenax virus 1 (strain <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x {82}(V)x(P)(P)xx(I)(X)xY(V)xxx(S)x(134)	YNU6_CAEEL CK: 431 len: 381 i P90444 caenorhabditis elegans. hypothetical  (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C  x(151)(I)X(P)(A)XX(L)(I)XXX(I)XXX(I)XXX(I)XXX(I)X(I)(I)X(P)(I)X(P)(I)X(P)(I)XXI(I)XXX(I)XX(	1,200 (L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,I)    11 (L)x(T)(I)xx(L)(S)(R)xx(M)xxx(L)x(309)   LIFVRASTLKTIILLSRIEMGRILEKPRILGTWSFTKIGLNCESLSGAIQR   IDGESEMIKKTKRALGYGENESIIVFLNKDR   EADQVLSTKEPHPLRYLQVEKVNEVFGFEETLVLPDHTLFLDSDPFSRHPP	<pre>&lt;(X){1,200}{L,I,V,M,A,P}X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,E,Y,W)(Q x(L)x(S)(L)xx(I)(S)(K)xx(V)xxx(S)x{153} MLRSLSTISKSTVRCMSLTSKMAAEQPSKQEVDDLFAEKPQHHNPEQRRHAYSVNKVELVGGVALD ck: 399 len: 336   P34542 caenorhabditis elegans. hypothetical</pre>	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{82}{A}x(S)(L)xx(L)(S)(K)xx(I)xxx(S)x(41) MMLINHTYKLLSYFLRKASNRFFNSSSSSFSCSFLVFLFVVFFSDCFFSITSFLISFGILSSFLIF ck: 5825 len: 170</pre>	ck: 7679 len: 69 ! P38469 marchantia polymorpha (liverwort). h <(X)[1,200](L,I,V,M,A,P)X(F,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(20)(I)x(P)(A)xx(F)(S)(H)xx(P)xxx(G)x[33) MASLESTERTOTELYPAHTETYPAHTESHEGPAFEGQALHLEGPGLGLEERNAHCHIFDNRKT MASLESTERTOTELYPAHTETYPAHTESHEGPAFEGQALHLEGPGLGLEERNAHCHIFDNRKT ck: 7226 len: 139 ! P53842 saccharomyces cerevisiae (baker's ye	<pre>ck: 8141 len: 79 ! P75677 escherichia coli. hypothetical 9.0 k &lt;(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(5)(L)x(P)(P)xx(F)(T)(R)xx(A)xxx(T)x(58) MTQSVLLPPGPFTRQAQAVTTTYSNITLEDDQGSHFRLVVRDTEGRMVWRAWNFEPDAGEGLN</pre>
<b>,</b>	μ	μ-	T Y MILEDTIKNWVG	<b>H</b>	FTIYAIL 1	1 1	1 NEGNAFLRADGR AGLPRLINTLRA	YP 1 KSQFIPSKDSVS	RGDFLYHSICNW RMAKARMILQKY
::	FF_	YRKG_BACSU 1:	YRBC_HAEIN 1: NWVGILNKQGIDTL	YR7B_ECOLI	YQ	ILCW	<pre>&lt;(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{138}(A)x(S)(P)xx(A)(T)(H)xx(A)xxx(C)x{117} SVPGDPIDILMQQLAILKQLLAHSAGRLRLCLSAADIERCREDKVLAMVAHIEGAGGFDGEGR RADGRRDSDTPLTIVRHIDYLINIMGEDHVALGSDEDGITLPDELGDV</pre> NTLRASGYDQLVLDKLLMRNWLRVLKNVWQQ	YPJG_BACSU  1: SKDSVSTPLTNGYIE YPQQ_KLEPN	x{156}(V)x(S)(L)xx(L)(C)(R)xx(V)xxx(P)x{113}  MKAPGLPADQOFFAIDLESGLYUNFQOLIGRWWFASOPASLFVGSLCIDFPRLDIVLRGEYGNLL RGDFLYHSICNWYQDNYAQPLTRESVAQFFNITPOHHLSKLFAQHGTMRFIEXVRWV RMAKARMILQKYHLSIHEVAQRCGFPDSDYFCRVFRRQFGLTPGEYSARFQG

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)(L)xx(L)(C)(R)xx(V)xxx(P)x{113}
DLFSGLVLNPQLLGRVWFASQPASLPVGSLCIDFPRLDIVLRGEYGNLL
LSKLFAQHGTMRFIEYVRWV
RQFGLTPGEYSARFQG
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1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
 x{99}(V)x(T)(L)xx(V)(S)(R)xx(S)x(249)
 1: MELSPNNSTDQSLLDAQLELWHTTFAFMKSMALKSAIHLRIADAIHLHGGAASLSQILSKVHLHPS
 GLASDSQLIVDVAIKQSAEVFOGISSLVDVGGGIGAAAQAISKAFFHYKCSVLDLA
 GVAKAFTHTDVQFIAGDMFESIPPADAVLLKSVLHDWDHDDCVKILKNCKKAIPPREAGGKVIIINMVVGAGPSDMKHKEMQAIFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKLOFVPIOSENIKEAFOSFKEGLKEIKINSFYLNAMFIMIIMALLWGVVYSYFP
IVSRFLGDGEIGNFILTFCIGFGGFIGAALVSKWGFNNNRGLTYFTVLSIVSLALFLFTPIFAVSVIAAILFFIAMEYGEVLAKVKVO
THE THE TAX OCCORDING CONTRACT TO SOLUTION OF THE THE THE TAX OCCORDING CONTRACT TO SOLUTION OF THE THE THE TAX OCCORDING CONTRACT TO SOLUTION OF THE TAX OCCORDING CONT
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SWISS-PROT, Release 38.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total sequences:
CPU time:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total finds:
Total length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _SEQUENCE 1.0
AAKG_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITIE: 95050763.

MEDITIE: 95050763.

MEDITIE: 95050763.

MICHELL B.J., WIDMER J., MITCHELHILL K., STAPLETON D., GAO G., MITTERS L.A., KEMP B.E.;

THE T., HOUSE C.M., WITTERS L.A., KEMP B.E.;

THE T., HOUSE C.M., WITTERS L.A., KEMP B.E.;

"Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are "Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are "Mammalian 5'-AMP-activated protein kinase ";

bomologs of proteins that interact with yeast snfl protein kinase.";

J. Biol. Chem. 269:29343-29345(1994).

"BIOL Chem. 269:29343-29345(1994).

"BIOL Chem. 269:29343-29345(1994).

"BIOL Chem. 269:29343-29345(1994).

"PROTEIN: AMP STAPL AND LARGE STYL-COA CARBOXYLASE. IT ALSO SYNTHESIS BY HOSPHORYLATION AND REGULATES CHOLESTEROL SYNTHESIS AVETABOLIC HYDROXYMETHYLGLUTARYL-COA REDUCTASE. APERABS TO ACT AS METABOLIC HYDROXYMETHYLGLUTARYL-COA REDUCTASE. APERABS TO ACT AS METABOLIC STRESS-SENSING PROTEIN KINASE SWITCHING OFF BIOSYNTHETIC PATHWAYS WHEN CELULAR ATP LEVELS ARE DEPLETED AND WHEN S'-AMP RISES IN WHEN CELULAR ATP LEVELS ARE DEPLETED AND WHEN S'-AMP RISES IN RESPONSE TO FUEL LIMITATION AND/OR HYPOXIA. THIS IS A REGULATORY RESPONSE TO FUEL LIMITATION AND/OR HYPOXIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1995 (Rel. 31, Created)
)1-FEB-1995 (Rel. 31, Last sequence update)
)1-FEB-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
5-AMMA-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN)
38 KD SUBUNIT) (FRAGMENTS).
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                                                                                                      DOMAIN
                                                                                                                                                                                                   SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT; A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
SUBUNIT FAMILY.
SIMILARITY: CONTAINS 4 CBS DOMAINS.
M: PEO0571: CBS: 1.
M: PEO0571: CBS: 1.
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                                                                     EMBL; U59433; AAC44308.1; ...
EMBL; D64116; BAA10975.1; ...
EMBL; D29112; CAB1465.1; ...
HSSP; PD2901; IACP;
SUBTILIST; B611536; ACPA,
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS0075; ACP_DOMAIN; 1.
PROSITE; P50075; ACP_DOMAIN; 1.
PRAM; PF00550; PP-binding; 1.
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15-JUL-1999 (Rel. 38, Last annotation update)
ACYL CARRIER PROTEIN (ACP)
ACPA OR ACPP
Bactllus subtilis
Bacillus subtilis
Bacillus/Staphylococcus group; Bacillus.
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SEQUENCE OF 1-17.

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SEQUENCE (PAIS1947).

REALTON M.P. AND AND SEC.;

REALTON M.P. AND AND SEC.;

REALTON M.P. AND SEC.;

11porteichoic acid.";

J. Bacteriol 176:681-690(1994).

J. Bacteriol 176:681-690(1994).

CHAIN IN FARTY ACID BIOSYNTHESIS.

CHAIN IN FARTY ACID BIOSYNTHESIS.

PATHMAY: KEY COMPONENT IN DE NOVO FARTY ACID BIOSYNTHESIS.

PATHMAY: KEY COMPONENT IN DE NOVO FARTY ACID BIOSYNTHESIS.

PATHMAY: KEY COMPONENT IN DE NOVO FARTY ACID BIOSYNTHESIS.

A'PHOSPHOPANTETHEINE PROSTHETIC GROUP.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 15-77, AND SEQUENCE OF 1-14 FROM STRAIN-168;
                                                                                                                                                                                                                                                                               MEDILINE; 96326321.
MORBIDONI H.R., DE MENDOZA D., CRONAN J.E.
"Bacillus subtilis acyl carrier protein is
liplid biosynthesis genes.";
J. Bacteriol. 178:4794~4800(1996).
                                                                                                                                                                                                     OGURO A., KAKESHITA H.,
Submitted (MAR-1996) to
                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
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the EMBL/GenBank/DDBJ databases
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AC O56346;
DT 15-DEC-1999 (Rel. 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila mojavensis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last seq
01-OCT-1996 (Rel. 34, Last ann
ALCOHOL DEHYDROGENASE 2 (EC 1.
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FROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_Short; 1.
PFAM; PF00663; adh_Short_C; 1.
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P09369;
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DATE BERROO

3.5.1.28).

Salmonella typhimurium. Bacteria; Proteobacteria;

gamma

subdivision;

Enterobacteriaceae;

AMIA\_SALTY STANDARD; PRT; 289 AA P33772; P33772; O1-FEB-1994 (Rel. 28, Created) O1-FEB-1994 (Rel. 28, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) PROBABLE N-ACETYLMURAMOYL-L-ALANINE AMIDASE

on update)

AMIA

PRECURSOR

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351 301 251 201

VERVYIR

DIGTPLRVTV WRAHTETHVG

GDRVTLFGPQ

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VRPGLLAYGY RAEDLQYTEM

APESVHPAVR QRAHFMHCVQ

ILPIGYADGV

CIGGKWYPVV TQVRAIKKIP

GAICMDQCVV

AGAYVSYQRL LCHPRAHFDM GVRAPILCLS TPTAEEISSL

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EACALVOMVC IEHRVHTVIS

ATPGLHLEGV ERAHIALIAR

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SEQUENCE 1.0

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ALR_TREPA
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                                                                                                                                                                                                                                                                                                                                                                                         "Partial sequence of alanine racemase from Treponema pallidum."; submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-ALANINE - D-ALANINE.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G., DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A., SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J., SOLZBERGEN E., HARDHAM J.M., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T. KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T. MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND HATCH B., HORST K., ROBERTS K., WAITHEY L., WEIDMAN J., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spirochete.";
Science 281:375-388(1998).
                                                                                                  SEQUENCE
                                                                                                                     BINDING
                                                                                                                                                    PFAM;
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51
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                                  MSRTRARVCL PVKADAYGHG
                                                                                                                       TE; PS00395; ALANINE_RACEMASE; FALSE_NEG PF00842; Ala_racemase; 1. erracemase; pyridoxal phosphate.
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Spirochaetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformaticy Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990
01-NOV-1990
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STYGENE; SG10008; AMIA.
PFAM; PF01520; Amidase_3; 1.
Hydrolase; Cell wall; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L19503; AAA27138.1; -.
                                                                                                                                                  MEDLINE; 91032898.

MEDLINE; 91032898.

"Nucleotide sequence of the Serratia marcescens SR50 chromosomal ampC "Nucleotide sequence of the Serratia marcescens SR50 chromosomal ampC beta-lactamase gene.";

FEMS Microbiol. Lett. 58:295-299(1990).

FEMS MICROBION: THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A SUBSTRATE SPECIFICITY FOR CEPHALOSPORINS.

-i- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)0 - A SUBSTITUTED BETA-
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SR50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serratia marcescens.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \vdash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: STRONG, TO B.SUBTILIS LYTC/CWLB.
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                                                                       SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNRGASSAMA KYLSERENRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSTFKLLKTL TSRRQVLKTG
                                                                                                                                AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLTLGSHILK KIKPIHKLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKTGSKRLVM LDPGHGGIDT GAIGRNGSQE
SWISS-PROT entry is copyright. It is produced een the Swiss Institute of Bioinformatics and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 37, Last annotation update)
ASE PRECURSOR (EC 3.5.2.6) (CEPHALOSPORINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35
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                                                           PERIPLASMIC (BY SIMILARITY)
O THE CLASS-C BETA-LACTAMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAALTLSGMS HAVAKEETLK TSNGHSKPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIISYFHWFD NQKAHTKKR
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PROBABLE N-ACETYLMURAMOYL-L-ALANINE
AMIDASE AMIA.

; 5F107FEC CRC32;
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        through a collaboration
d the EMBL outstation -
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SON SETTINGS
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  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   SEQUENCE FROM N.G.
SEQUENCE FROM N.G.
SEQUENCE FROM N.G.
SETRAIN-OSSO, AND 14;
MEDLINE, 9319292.
KOPP U., WIEDEMANN B., LINDQUIST S., NORMARK S.;
KOPP U., WIEDEMANN B., LINDQUIST S., NORMARK S.;
Requences of wild-type and mutant ampb genes of Citrobacter
"Sequences of cidcae.";
and Enterobacter Cloacae.";
antimicrob. Agents Chemother. 37:224-228(1993).
Antimicrob. Agents Chemother. 37:224-228(1993).
Antimicrob. Agents Chemother. 37:224-228 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
ACT_SITE
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 1.0
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PROSITE; PS00336; BETA_LACTAMASE_C; 1.

PFAM; PF00144; beta-Lactamase; 1.

Hydrolase; Antibiotic resistance; Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351
                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel.
01-APR-1993 (Rel.
01-JUN-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; P.
Citrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMPD_CITER
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EMBL; Z14002; CAA78390.1;
EMBL; Z14003; CAA78391.1;
PIR; A48901; A48901.
PIR; S26138; S26138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      itrobacter freundii, and
acteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S11710; QKSE.
A48176; A48176.
                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLANKWFPND
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79
328
376 AA;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacter cloacae.
gamma subdivision; Enterobacteriaceae;
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BY SIMILARITY.
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(See http://www.isb-sib.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminus.
EMBL; M58575; AAA49664.1;
EMBL; M58576; AAA49665.1;
EMBL; M60769; AAA49886.1;
PIR; JQ1298; JQ1298.
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                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the Ewp pron-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 92009222.
GERKE V., KOCH W., THII
"Primary structure and annexin II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92011609.
IZANT J.G., BRYSON L.J.;
"Xenopus annexin II (calpactin I) heavy
terminus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-MAR-1992 (Rel. 21, Created)
Ol-ANG-1992 (Rel. 23, Last sequence update)
Ol-CT-1994 (Rel. 30, Last annotation update)
ANNEXIN II TYPE II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN)
(CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN
IV) (PAP-IV):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-OOCYTE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
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                                                                                                                                                                                                            SUBSTANTIALLY.

DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.

MISCELLANEOUS: IT MAY CROSS-LINK FLASMA MEMBRANE PHOSPHOLIPIDS
WITH ACTIN AND THE CYTOSKELETON AND BE INVOLVED WITH EXOCYTOSIS.
SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                  RE 100:259',264(1991).

RE 100:259',264(1991).

RETURITY FOR CALCIUM IS GREATLY ENHANCED BY ANIONIC PHOSPHOLIPIDS. APPINITY FOR CALCIUM IS GREATLY ENHANCED BY ANIONIC PHOSPHOLIPIDS. IT BINDS TWO CALCIUM IONS WITH HIGH AFFINITY.

SUBGUST: TETRAMER OF 2 LIGHT CHAINS (P10 PROTEINS) AND 2 HEAVY CHAINS (P36 PROTEINS).

SUBCELLULAR LOCATION: IN THE LAMINA BENEATH THE PLASMA MEMBRANE. SUBCELLULAR LOCATION: IN THE LAMINA BENEATH THE WISSME AMBRICATIVE ADULT BRAIN, HEART, STRIATED MUSCLE, LIVER, KIDNEY, AND VERY HIGH LEVELS IN SKIN.

EVELOPMENTAL STAGE: THROUGHOUT OCCENESIS AND IN MATURE EGGS. CONSTANT LEVELS DURING EARLY EMBRYOGENESIS, BUT DECREASE AT 8H. ATTER MIDBLASTULA TRANSITION, THE STEADY STATE LEVEL INCREASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S26139; S26139
ENCE 187 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EL C.; expression of the Xenopus laevis gene
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Xenopodinae;
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IIAA_SEQUENCE 1.0

IID ARG1_XENLA
AC Q91553;
DT Q1-NOV-1997 (R
DT 01-NOV-1997 (R
DT 01-NOV-1997 (R
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                                                                                                                                                                                                                                                                                                                                                                         AC TISSUE-INTESTINE;

XX MEDLINE; 95014323.

XA PATTERTON D., SHI Y.-B.;

XA PATTERTON D. SHI Y.-B.;

XA PATTERTON D. SHI Y.-B.;

YEL J. B.101. Chem. 269:25328-25334(1994).

Y. B.101. Chem. 269:25328-25334(1994).

C -!- FUNCTION: AS WELL AS ITS ROLE IN THE UREA CYCLE, MAY BE INVOLVED IN TISSUE REMODELING.

C -!- CATALYTIC ACTIVITY: L-ARGININE + H(2)O = L-ORNITHINE + UREA.

C -!- CATALYTIC ACTIVITY: L-ARGININE DEGRADATION.

C -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

C -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

C -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED AT DIFFERING TADPOLE STAGES IN TAIL,

TRIESTINE, HINDLIMB AND TRUNK REGION. MOST ABUNDANT IN TADPOLE

TAIL.

TAIL

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HSSP; P04083; 1B09.
PROSITE; P500223; ANNEXIN; 4.
PRAM; PF00191; annexin; 4.
PFAM; PF00191; annexin; 4.
PFAM; PF00191; annexin; 4.
PFAM; PF00191; annexin; 4.
PF00191; ANNEXIN; ANNEXIN; 4.
PF00191; ANNEXIN; 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
ARGINASE, NON-HEPATIC 1 (EC 3.5.3.1).
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                                DEVELOPMENTAL STAGE: FIRST DETECTED IN NEURULA (STAGE 16/17).
HIGHEST LEVELS IN WHOLE TANDFOLE FOUND BAROUND STAGE 47/48. IN THE
INTESTINE, INCRASASED LEVELS ARE FOUND DURING METAMORPHOSIS: (STAGES
58-64). LOW LEVELS EXPRESSED IN HINDLIMB UNTIL STAGE 66 AFTER
WHICH, LEVELS DRAMATICALLY INCREASE. IN THE TAIL, A CONSTANT HIGH
LEVEL OF EXPRESSION IS FOUND THROUGHOUT METAMORPHOSIS.
INDUCTION: ACTIVATED BY THYROID HORMONE (T3).
SIMILARITY: BELONGS TO THE ARGINASE FAMILY.
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B41002;
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Xenopodinae;
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METAMORPHOSIS.
INDUCTION: ACTIVATED
SIMILARITY: BELONGS

ACTIVATED BY THYROID HORMONE (T3).

BELONGS TO THE ARGINASE FAMILY.

INTESTINE, INCREASED LEVELS ARE FOUND DURING METAMORPHOSIS (STAGES 58-64) AND IN THE HINDLIMB, EXPRESSED AT LOW LEVELS DURING METAMORPHOSIS UNTIL STAGE 66 WHEN LEVELS DRAMATICALLY INCREASE. IN THE TAIL, A CONSTANT HIGH LEVEL OF EXPRESSION IS FOUND THROUGHOUT

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ARG1_XENLA
                                             SEQUENCE FROM N.A.

TISSUE-INTESTINE;

K MEDLINE; 95014323.

A PATTERTON D., SHI Y.-B.;

TAPYIOID hormone-dependent differential regulation of my ribyroid hormone-dependent in THE UREA CYCLE, MAINTING TISSUE REMODELING.

-I- CAPALYTIC ACTUTTY: L-ARGININE + H(2)O = L-ORNITHING TADACTOR: MANGANESE (BY SIMILARITY).

-I- CAPALYTIC HOROTRIMER (BY SIMILARITY).

-I- PATHWAY: FIRST STEP IN ARGININE DEGRADATION.

-I- PATHWAY: FIRST STEP IN ARGININE DEGRADATION.

-I- TISSUE SPECIFICITY: EXPRESSED AT DIFFERING TADPOLE:

TAIL, INTESTINE, HINDLIMB AND TRUNK REGION. STRONGE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sand
01-NOV-1997 (Rel. 35, Last and
ARGINASE, NON-HEPATIC 2 (EC 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1.0
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Multigene f
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
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DEVELOPMENTAL STAGE: FIRST DETECTED IN NEURULA (STAGE HIGHEST LEVELS IN WHOLE TADPOLE FOUND AROUND STAGE 47,
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ane family.
122 MANGANESE 1 (BY SIMILARITY).
145 145 MANGANESE 1 AND 2 (BY SIMILARITY).
147 147 MANGANESE 2 (BY SIMILARITY).
149 149 149 MANGANESE 1 (BY SIMILARITY).
253 253 MANGANESE 1 AND 2 (BY SIMILARITY).
254 255 MANGANESE 2 (BY SIMILARITY).
255 255 MANGANESE 2 (BY SIMILARITY).
256 255 MANGANESE 2 (BY SIMILARITY).
257 258 MANGANESE 2 (BY SIMILARITY).
258 259 MANGANESE 2 (BY SIMILARITY).
259 250 MANGANESE 3 (BY SIMILARITY).
250 251 MANGANESE 3 (BY SIMILARITY).
250 251 MANGANESE 3 (BY SIMILARITY).
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annotation
C 3.5.3.1)
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ANAGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).
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ARG2_XENLA Length: 360
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                                                                                                                                                                                     _SEQUENCE 1.0

ARG3_XENLA
O9155;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
ARGINASE, NON-HEPATIC 3 (EC 3.5.3.1).
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HSSP; P07824; ZRLA.
PROSITE; PS00147; ARGINASE_1; 1.
PROSITE; PS00148; ARGINASE_2; 1.
PROSITE; PS00153; ARGINASE_3; 1.
PFAM; PF00491; arginase; 1.
PFAM; PF00491; Arginase metabolism; Hydrolase;
Urea cycle; Arginine metabolism; Hydrolase;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Xenopodinae;
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                                                                                                                                                                                     P11446;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1988 (Rel. 37, Last annotation update)
N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.
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HSSP, P07824; 2RLA
PROSITE; PS00147; ARGINASE_1;
PROSITE; PS00148; ARGINASE_3;
PROSITE; PS01053; ARGINASE_3;
PFAM; PF00491; arginase; 1.
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SEQUENCE FROM N.A. MEDLINE; 89121510.
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PATHWAY: FIRST STEP IN ARGINIED DEGRADATION.

SUBUNIT: HOMOTRIMER (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED AT DIFFERING TADPOLE STAGES IN TAIL.

TAIL. INTESTINE, HINDLIMB AND TRUNK REGION. STRONGEST IN TADPOLE TAIL.

DEVELOPMENTAL STAGE: FIRST DETECTED IN EARLY TAILBUD (STAGE 23/24). HIGHEST LEVELS IN WHOLE TADPOLE FOUND AROUND STAGE 47/48.

IN THE INTESTINE, INCREASED LEVELS ARE FOUND DURING METAMORPHOSIS IN THE INTESTINE, INCREASED LEVELS ARE FOUND DURING METAMORPHOSIS.

(STAGES 58-64) AND IN THE HINDLIMB, EXPRESSED AT LOW LEVELS DURING METAMORPHOSIS UNTIL STAGE 66 WHEN LEVELS DRAMATICALLY INCREASE. IN THE TAIL, A CONSTANT HIGH LEVEL OF EXPRESSION IS FOUND THROUGHOUT THR
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SIMILARITY: BELONGS TO THE ARGINASE FAMILY.
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                                                                                                                        subdivision; Enterobacteriaceae
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THQYPELLEQ

NATSGVSGAG

NKLKEANLIA RKAAISNSFC ETITCRLKSG 51

QLKGIVDLPL QPMSDISEFS

PGVDVVFLAT

AHEVSHDLAP

AGKLISDLHP QFLEAGCVVF

ATFYEKYYGF LALKPLIDAD MLNTLIVGAS

GYAGAELVTY

VNRHPHMNIT ALTVSAQSND

251

VTQAQVAQVL QQAYAHKPLV RLYDKGVPAL KNVVGLPFCD

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ARGC_ECOLI
                                                              STREATE TRANSPORTED COLOR COLO
                                                                                        EMBL; M21446; AAA23477.1; -.

EMBL; J01587; AAB59146.1; -.

EMBL; J010006; AAC43664.1; -.

EMBL; U00006; AAC43664.1; -.

EMBL; D00006; AAC43664.1; -.

EMBL; D00006; AAC76940.1; -.

PIR; JT0332; RDECEP.

ECOGENE; EG10065; ARGC.

PROSITE; PS01224; ARGC; 1.

PFAM; PF01118; Semialdhyde_dh; 1.
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Gene 68:275-283(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEINNEL T., SCHMITT E., MECHULAM Y., BLANQUET S.;

Structural and biochemical characterization of the Escherichia arge gene product.";

J. Bacteriol. 174:2323-2331(1992).

-I. CATALYTIC ACTIVITY: N-ACETYL-1-GLUTAMATE 5-SEMIALDEHYDE + N-ACETYL-5-GLUTAMYL PHOSPHATE + NADPH.

-I. PARHWAY: THIRD STEP IN ARGININE BIOSYNTHESIS.

-I. SIMILARITY: TO OTHER BACTERIAL ARGC AND TO NAGSA DOMAIN OF PROTEIN ARG5,6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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PIETTE J., CUNIN R., BOYEN A., CHARLIER D.R.M., CRABEEL M.,

VAN VLIET F., GLANSDORFF N., SQUIRES C., SQUIRES C.L.;

"The regulatory region of the divergent argECBH operon in Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 94089392,
BLATTNER F.R., BURLAND V.D.,
DANIELS D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-19
STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-48 FROM N.A. STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 10:8031-8048(1982).
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"Analysis of the Escherichia coli genome. IV. DNA sequence region from 89.2 to 92.8 minutes.";
Length: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92202162
                                                              334 AA;
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                                                       154 E
; 35952 MW;
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21:5408-5417(1993).
February 14, 2000 08:02
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                                                                  DB98AB60 CRC32;
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Type: P
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   Check:
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C:- FUNCTION: THIS PROPORENT (FO) OF MITOCHONDRIAL ATPASE.
C:- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CP(1) - THE CATALYTIC
C:- CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
C:- CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
C:- HAS THREE MAIN SUBUNITS: A, B AND C.
C:- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE.
C:- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE.
C:- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE.
C:- SUBCELLANEOUS: THESE PROTEIN STORED IN THE
C:- STORAGE BODIES OF ANIMALS OR HUMAN AFFECTED WITH CEROID
LIPOFUSCINOSIS (BATTEN'S DISEASE).
C:- MITOCHONDRIAL ATP SYNTHASE PROTECLIPID AND THEY SPECIFY PRECURSORS
WITH DIFFERENT IMPORT SEQUENCES BUT IDENTICAL MATURE PROTEINS.
C:- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ATP SYNTHASE LIPID-BINDING PROTEIN P3 PRECURSOR (EC 3.6.1.34) (ATPASE PROTEIN 9) (SUBUNIT C).
ATPSG3.
                                                                                                                                                                                                                                                        SEQUENCE 1.0
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YAN W.L., LERNER T.J., HA
"Sequence analysis and ma
synthase subunit 9 cDNA (
Genomics 24:375-377(1994)
                                                                                                                                                                                                                                                                                                                    101
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Podospora anserina Mitochondrion.
                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1993 (Rel. 38, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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**ROSITE; PS00605; ATPASE_C; 1.

**PAM; PF00137; ATP-synt_C; 1.

**Yorogen ion transport; Lipid-binding; Mitochondrion; 
**Transit peptide; Multigene family; Transmembrane.

**Transit peptide; Multigene family; Transmembrane.

**Transit peptide; Multigene family; Transmembrane.

**Transit peptide; Mitochondrion; 
**Tran
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                                                                                                                                                                                                                                                                                                                 QQLFSYAILG
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mapping of a )
NA (ATP5G3).";
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                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000 08:02 Type: P
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mitochondrial
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II AA_SEQUENCE 1.0

IID ATP8_PONDA
AC P9269;
AC P9269;
DT 01.NOV-1997 (F
DT 15-UIL-1999 (F
DT 15-UIL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP8_PODAN Length: 50
                                                                                                                                                                                                                                                                                                                                                                                 XU X., ARNASON U.;

The mitochondrial DNA molecule of Sumatran orangutan and a molecular proposal for two (Bornean and Sumatran) species of orangutan.";

J. Mol. Evol. 43:431-437(1996).

J. FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.

-!- SUBCELIULAR LOCATION: MEMBRANE-BOUND.
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TRANSMEM
SEQUENCE
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STRAINS;
MEDILINE; 90291512.
CUMMINGS D.J., MCNAILY K.L., I
The complete DNA sequence of
anserina.";
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYN (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEY:
-i- SUBCILIULAR LOCATION: MEMBRANE-BOUND.

-i- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fu
Sordariales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pongo pygmaeus abelii (Sumatran Mitochondrion.
Mitochondrion.
Eukaryota; Metazoa; Chordata; C)
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X55026; CAA38808.1; --
Hydrogen ion transport; CF(0); Mitochondrion;
TRANSMEM 13 32 POTENTIAL.
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                                                            EMBL; x97707; CAA66287.1; -.
PFAM; PF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-YN93-312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (AGL).
MTATP8 OR ATP8.
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s; Sordariaceae; Pod
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          ΑĄ;
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              7860 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D3E7DF1F CRC32;
              B5CEA057
                                          POTENTIAL
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                 CRC32;
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ATP8\_PONPA

Length: 68

February

14,

2000 08:02

Type:

ש

3336

MPQLNTTTWP

TIITPMLLAL

FLITQLKLLN

SHLHPPTPPK

FTKPKLHAKP

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SEQUENCE FROM N.A.

***REDLINE; 95132634.**

***A HORAI S., HAYASAKA K., KONDO R., TSUGANE K., TAKAHATA N.;

***T "Recent African origin of modern humans revealed by complete sequence of the microchondrial DNAs.";

**T of hominoid microchondrial DNAs.";

**CC Natl. Acad. Sci. U.S.A. 92:532-536(1995).**

**CC Natl. Acad. Sci. U.S.A. 92:532-536(1995).**

**CC Natl. Acad. Sci. U.S.A. 92:532-536(1995).**

**CC ONTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPLEX.**

**CC (CF(O) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.**

**CC OTHECELLULAR LOCATION: MEMBRANE-BOUND.**

**CC OTHECELLULAR LOCATION: MEMBRANE-BOUND.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP8_PONPP
                                                                                                                                                                                                                                                                                                                                                                             _SEQUENCE 1.0
ATP8_PONPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrogen ion TRANSMEM 5EQUENCE 68
                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
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Eutheria; Primates;
                                                                                                                                                                                                                                                  Pongo pygmaeus (Orangutan). Mitochondrion.
                                                                                                                                                                                                                                                                                  MTATP8 OR ATP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XUX., ARNASON U.;
"The mitochondrial DNA molecule of Sumatran orangutan and a molecular proposal for two (Bornean and Sumatran) species of orangutan.";
J. MOL. Evol. 43:431-437(1996), EVOL. Evol. 43:431-437(1996), THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0)) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.

-!- SUBCELULAR LOCATION: MEMBRANE-BOUND.
-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
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Mitochondrion.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
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pF00895; ATP-synt_8; 1.
ygen ion transport; CF(0); Mitochondrion;
ygen ion transport POTENTIAL.
ynem 24 POTENTIAL.
ynem 7 7910 MW; 8AAC1F6C CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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Catarrhini; Hominida
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Catarrhini; Hominidae; Pongo.
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                                                                                                                                                                                                                Hominidae;
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                                                                                                                              sequences
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SUBCELLULAR SIMILARITY:

SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its

LOCATION: MITOCHONDRIAL.
BELONGS TO THE ATPASE EPSILON CHAIN FAMILY.

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!!AA_SEQUENCE 1.0
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                                                                                                                                                                  MEDLINE; 93162045.

MEDLINE; 93162045.

ROCHSTRASSER D.F., FRUTIGER S., PAQUET N., BAIROCH A., RAVIER F., PASQUALI C., SANCHEZ J.-C., TISSOT J.-D., BJELLQVIST B., VARGAS R., PASQUALI C., SANCHEZ J.-C., TISSOT J.-D., BJELLQVIST B., VARGAS R., PAPEL R.D., HUGHES G.J.;

"Human liver protein map: a reference database established by microsequencing and gel comparison.";

Electrophoresis 13:992-1001(1992).

-I-FUNCTION: PRODUCES ATP FROM ADD IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.

-I-SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALUTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) SEEMS TO HAVE NINE SUBUNITS: A, B, C, D, E, F, G, F6 AND 8 (OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

LAMBERDIN J.E., MCCREADY P.M., SKOWRONSKI E., ADAMSON A.W.,

BURKHART SCHUITZ K., GORDON L., KYLE A., RAMIREZ M., STILWAN

PHAN H., VELASCO N., GARNES J., DANGANAN L., POUNDSTONE P.,

CHRISTENSEN M., GEORGESCU A., AVILA J., LIU S., ATTIX C., A

TRANKHEIM M., AMICO-KELLER G., COEFIELD J., DUARTE S., LUCA

BRUCE R., THOMAS P., QUAN G., KRONMILLER B., ARELLANO A.,

MONTGOMERY M., OW D., NOLAN M., TRONG S., KOBAYASHI A., OLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LI
MEDLINE;
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MEDITINE, 92182007.

JORDAN E.M., BREEN G.A.M.;

Molecular cloning of an import precursor of human mitochondrial ATP synthase complex.";

human mitochondrial ATP synthase romplex.";

human mitochondrial ATP synthase romplex.";
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HOMO Sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P30049;
01-ARR-1993 (Rel. 25, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation updat
ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MONTGOMERY M., OW D.,
CARRANO A.V.;
Submitted (FEB-1998) t
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PFAM; PF00895; ATP-synt_8;
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00895; AFF-Synt_8; 1.
10n transport; CF(0); Mitochondrion;
10n transport CF(0); MITOCHONDRION;
10n transport; CF(0); MITOCHONDRION;
10n transport CF(0); MITO
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MITOCHONDRIAL PRECURSOR (EC 3.6.1.34).
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STITE DESCRIPTION OF THE PROPERTY OF THE PROPE
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or send a
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MEDITINE; 88163679.

OHTA S., YOHDA M., ISHIZUKA M., HIRATA H., HAMAMOTO T.,

OHTAWARA-HAMAMOTO Y., MATSUDA K., KAGAWA Y.;

"Sequence and over-expression of subunits of adenosine triphosphate
synthase in thermophilic bacterium PS3.";

synthase in thermophilic bacterium PS3.";

BIOCHIM. BLOPHYS. Acta 933:141-155(1988).

FUNCTION: A POSSIBLE FUNCTION FOR THIS PROTEIN IS TO GUIDE THE
ASSEMBLY OF THE MEMBRANE SECTOR OF THE ATPASE ENTRY COMPLEX.

-I- SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.
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EMBL; X63423; CAA45017.1; -.
EMBL; AC004721; AAC04304.1; -.
PIR; S22348; S22348.
PIR; S22348; S2348.
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMBL outstation its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MNOV-1997 (Rel. 35, Last annotation update)
ATP SYNTHASE PROTEIN I.
Bactllus P53 (Thermophilic bacterium P5-3).
Bacteria; Firmicuttes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
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ATP synthesis; CF(1); Hydroglase;
Mitochondrion; Transit peptide.
TRANSIT 1 22 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                  EMBL; X07804; CAA30647.1; -. 
PIR; S01397; S01397; S01397; Hydrogen ion transport; CF(0); 
SEQUENCE 127 AA; 14595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 60
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                                                                                                                                                                                      MGNLQAMFWR
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168 AA;
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                                                                                                                                  QAVAARKKVR
                                                                                                                                                                                          QVRYILYLLA
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17490 MW;
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PRT;
                                                                                                                                                                                                                                                                                                  Transmembrane. 5999D881 CRC32;
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398
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BMPA_XENLA
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EMBL; X63424; CAA45018.1; -.
PIR; S16244; S16244
PIR; JH0687; JH0687;
HSSP; P18075; 1BMP.
PROSITE; PS00250; TGF_BETA; 1.
PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide; 1.
S1gnal; Growth factor; Cytokine; Bon S1gnal; Growth factor; Cytokine; Bon S1GNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P25703;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
01-JUL-1993 (Rel. 26, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2-I PRECURSOR (BMP-2-I).
Xenopus laevis (African clawed frog).
Yenopus laevis (African clawed frog).
                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsendan.email.tolicense@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLLINE; 91274367.

PLESSOW S., KOESTER M., KNOECHEL W.;

"CDNA sequence of Xenopus laevis bone morphogenetic
(BMP-2).";
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SLTPDKDNWP QIRPLLYTFS HDGKGHALHK RQKRQARHKQ
                                                                                                   FELRLLSMFG LKRRPTPGKN VVIPPYMLDL YHLHLAQLAA
                                                                                                                           MVAGIHSLLL LLFYQVLLSG CTGLIPEEGK RKYTESGRSS
                                                 ELRIFREQVQ
                                                                                                                                                    Length: 398 February 14, 2000 08:02
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                        VTPAIARWIA HKQPNHGFVV
                                                 EPFESDSSKL HRINIYDIVK
                                                                                                                                                                              45575 MW;
                                                                                                                                                                           INTERCHAIN (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
POTENTIAL.
S > P (IN REF. 2).
V -> L (IN REF. 2).
N -> T (IN REF. 2).
N -> T (IN REF. 2).
                                                                           EEIPESREKT
                                                                                                                                                                                                                                                                              POTENTIAL.

BONE MORPHOGENI
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                           Bone; Cartilage; Glycoprotein
                                                                                                                                                                                                                                                                                                                        MORPHOGENETIC
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                                                   PAAAASRGPV
                                                                         IORFFFNLSS
                                                                                                                                                    Type: P Check:
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                                                 VRLLDTRLVH
                                                                                                    DEGTSAMDFQ
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301

HPLYVDFSDV GWNDWIVAPP GYHAFYCHGE CPFPLADHLN STNHAIVQTL

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!!AA_SEQUENCE 1.0
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Growth
SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISHIMATSU S., SUZUKI A., SHODA A., MURAKAMI K., UENO N., NISHIMATSU S., SUZUKI A., SHODA A., MURAKAMI K., UENO N., "Genes for bone morphogenetic proteins are differentially in early amphibian embryos.",
Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LIMBED.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LIMBED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X63425; CAA45019.1; -. PIR; JH0688; JH0688. HSSP; P18075; 1BMP
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2-II PRECURSOR (BMP-2-II)
Energyota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 92378616.
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PF00019; TGF-beta; 1.

PF00688; TGFb_Propeptide; 1.

1; Growth factor; Cytokine; E
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                                       ACCVPTELSA ISMLYLDENE KVVLKNYQDM VVEGCGCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284
398
363
395
397
397
362
137
202
237
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                                                                                    GYHAFYCHGE CPFPLADHLN STNHAIVQTI
                                                                                                                                              HDGKGHALHK
                                                                                                                                                                                                  HKQPNHGFVV
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                                                                                                                                                                                                                                                                                                                                                                                                          CTGLVPEEGK
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POTENTIAL.

BONE MORPHOGENETIC PROTEIN 2
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                              EVTHLDNDTN
                                                                                                                                                                                                                                               PAAAASRGPV
                                                                                                                                                                                                                                                                                                                                                      YHLHSAQLAD
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                                                                                                                                                                                                                                           DRJA_HUMAN STANDARD; PRT; 423 AA.

Q01851; Q15318; Q14986;
Q1-VUL-1993 (Rel. 26, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
Q1-NOV-1997 (Rel. 26, Created)
Q1-NOV-1997 (Rel. 26, Cre
XIANG M., ZHOU L.-J., MACKE J.P., EDDY R.L., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
                                                                                            SEQUENCE FROM N.A. TISSUE-RETINA;
                                                                                                                                                                                        Eutheria; Primates;
[1]
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ACT_SITE
SEQUENCE
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HSSP; P47227; 1BDB.
PROSITE: P5000061; ADH_SHORT; 1.
PFAM, PF00106; adh_Short; 1.
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FURUKAWA K., ARIMURA N., MIYAZAKI T.;

"Nucleotide sequence of the 2,3-dihydroxybiphenyl dioxygenase gene of pseudomonas pseudoalcaligenes.";

J. Bacteriol. 169:427-429 (1987).

1- PANHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO BENZOIC ACID AND CHLOROBENZOIC ACIDS.

2-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BPHB_PSEPS STANDARD; PRT; 275 AA.

P08694;

01-VAN.1988 (Rel. 06, Created)

01-NOV-1991 (Rel. 20, Last sequence update)

01-OCT-1996 (Rel. 34, Last annotation update)

BIPHENYL-2,3-DIHYDRO-2,3-DIOL DEHYDROGENASE (EC 1.3.1.-) (BIPHENYL-CIS-DIOL DEHYDROGENASE) (2,3-DIHYDROXY-4-PHENYLHEXA-4,6-DIENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aromatic hydrocarbons catabolism; Oxidoreductase; NAD NP_BIND 9 3 NAD (BY SIMILARITY).
SECULENCE 153 153 BY SIMILARITY.
SECULENCE 275 AA; 28726 MW; EA999DF7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria; gamma subdivision;
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                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRGNVIFTIS
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SHOWS T.B., NATHANS J.;
J databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
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SEQUENCE FROM N.A.

MEDILINE; 94052142.

MEDILINE; 94052142.

MEDILINE; 94052142.

BHARRAVA A.K., LI Z., WEISSMAN S.M.;

BHARRAVA A.K., LI Z., WEISSMAN S.M.;

BHARRAVA A.K., LI Z., WEISSMAN S.M.;

Therefore the POU family of proteins in accivated and phorbol 12-myristate 13-accetate-treated proteins in accivated and phorbol 12-myristate 13-accetate-treated Jurkat T cells.";

Jurkat T acad. Sci. U.S.A. 90:10260-10264(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developing mammalian nervous system.";

Nucleic Acids Res. 20:4919-4925(1992).

-i- fUNCTION: PROBABLE TRANSCRIPTION FACTOR WHICH MAY PLAY A ROLE IN FUNCTION: PROBABLE TRANSCRIPTION FACTOR WHITHIN A SUBSET OF THE REGULATION OF SPECIFIC GENE EXPRESSION WITHIN A MAINTAINING THE DENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

-i- SUBCELLULAR LOCATION: NUCLEAR.

-i- TISSUE SPECIFICITY: BRAIN. SEEMS TO BE SPECIFIC TO THE RETINA. PRESENT IN THE DEVELOPING BRAIN, SPINAL CORD AND EXE.

-i- DEVELOPMENTAL STAGE: EXPRESSION PEAKS EARLY IN EMBRYOGENESIS (DAY 13.5) AND IS UNDETECTABLE 14 DAYS AFTER BIRTH.

-i- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
  CONFLICT
                                                                                                                                                                                             DNA_BIND
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U10063; AAA57161.1; -.
EMBL; U10062; AAA57161.1; JOINED.
EMBL; L20433; AAA65605.1; -.
EMBL; X64624; CAA45907.1; -.
HSSP, P10037; 1AU7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLLUM R.G., FISHER P.E., DATTA M., MELLIS HUBBNER K., CROCE C.M., ISRAEL M.A., THEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00035; POU_1; 1.
PROSITE; PS00465; POU_2; 1.
PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00046; homeobox; 1.
PFAM; PF00157; pou; 1.
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PS00027; HOMEOBOX_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                              regulation;
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      WW.
                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; DNA-binding; Homeobox;
                                                                   A > R (IN REF. 1).

AGAG -> ARR (IN REF. 3).

MISSING (IN REF. 3).

MISSING (IN REF. 3).

GP -> AR (IN REF. 3).

GP -> PR (IN REF. 3).

GP -> AA (IN REF. 3).

GP -> AA (IN REF. 3).

A -> S (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 3).
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GS (IN R)
PS (IN R)
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                                                                                                               BR3A_HUMAN Length: 423
                                                                            BRA1_BRAFL
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Q17134;
Q1-137 (Rel.
01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
BRACHYURY PROTEIN I
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                                                                                                                                                                                                                                    EMBL; X91903;
HSSP; P24781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                         MSSAETMKQP
                                                                          Length: 448
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                                         TAASPDQFSV SHLLSAVESE ISAGSEKGDP
                                                                            February 14, 2000
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NVVRVWFCNQ ROKOKRMKFS
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STANDARD;
                                                   RKRTSIAAPE
                                                                        STICRFESLT
                                                                                             SICDSDTDPR
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                                                                                                                                      GPGGGGPGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTEL INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES REQUIRED FOR MESODERM FORMÁTION AND DIFFERENTIATION (BY SIMILARITY).

1. SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

1. DEVELOPMENTAL STAGE: FIRST DETECTED IN THE 10 H GASTRULA AROUND THE BLASTOPORE. IN LATER STAGES OF GASTRULATION AND EARLY NEURALIZATION, EXPRESSED IN POSTERIOR MESODERM AND THE NOTOCHORD WHERE EXPRESSION CONTINUES AT LEAST UNTIL SWIMMING LARVAL STAGE.

1. SIMILARITY: CONTAINS A T-BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96125169.

HOLLAND P.W.H., KOSCHORZ B., HOLLAND L.Z., HERRMAN "Conservation of Brachyury (T) genes in amphioxus developmental and evolutionary implications."; Development 121:4283-4291(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Branchiostoma floridae (Florida lancelet) (Amphioxus)
Eukaryota; Metazoa; Chordata; Cephalochordata; Branch
                                                                      PROSITE; PS01264; TBOX_2; 1.
PROSITE; PS01283; TBOX_1; 1.
PFAM; PF00907; T-box; 1.
Developmental protein; Transcription regulation; DNA-binding;
Developmental protein; Multigene family.
                                                                                                                                                                                                                                                                        CAA62999.1; -.
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35, Last sequence update)
35, Last annotation update)
HOMOLOG 1 (AMBRA-1)
                  49253 MW;
T-BOX.
; 5948F2D3 CRC32;
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AC P33967;
DT 01-FEB-1994 (Rel. 2
DT 01-FEB-1994 (Rel. 2
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-!- TISSUE SPECIFICITY: MESODERM AND NOTOCHORD.
-!- SIMILARITY: CONTAINS A T-BOX DOMAIN.
HSSP: P24781; 1XBR.
HSSP: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96125169.

HOLLAND P.W.H., KOSCHORZ B., HOLLAND L.Z., HERRMANN B.G.;

"Conservation of Brachyury (T) genes in amphioxus and ver
developmental and evolutionary implications.";

Development 121:4283-4291(1995).

Development 121:4283-4291(1995).

FEQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION

REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BRACHYURY PROTEIN HOMOLOG 2 (AMBRA-2).
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Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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                                                                                                        STANDARD;
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                                                                                                                                                                                                            DSGYGHSTTP PAPQTRITSN NWSPMTMPSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAFLDAKERN DTKSGHDDLT DQQPQFSQLG
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28, Created)
28, Last sequence update)
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48469 MW; 4828EB28 CRC32;
                                                                                                                                                                                                                                                                                                                                                     THUMLSMSAM PHTTTSTHAQ YPNLWSVSNN
                                                                                                                                                                                                                                                                                                                                                                                                                         DRYSTLRNHR
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                                                                                                        PRT;
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vertebrates:
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Hydrolase; Zinc.
METAL 59
METAL 100
METAL 103
                                                                                                                                                                                                                                                                                                                                           **ROBAYASHI K., KAMAKURA T., TANAKA T., YAMAGUCHI I., ENDO T.;

**PNUCLEOCTICLE Sequence of the bsr gene and N-terminal amino acid

sequence of blasticidin S deaminase from blasticidin S resistant

Escherichia coli TK121.";

Agric. Biol. Chem. 55:3155-3157(1991).

-I- PUNCTION: CATALYSES THE DEAMINATION OF THE CYTOSINE MOIETY OF THE

ANTIBIOTICS BLASTICIDIN S, CYTOMYCIN AND ACETYLBLASTICIDIN S.

-I- CATALYTIC ACTIVITY: BLASTICIDIN S + H(2)O =

DEAMINOPURDROXYBLASTICIDIN S + NH(3).

-I- COFACTOR: ZINC (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES

-I- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                EMBL; S81409; AAC60404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K55-S1;
MEDLINE; 92144117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last annotation update) BLASTICIDIN-S DEAMINASE (EC 3.5.4.23).
                                                                                           PFAM; PF00383; dCMP_cyt_deam; 1.
                                                                                                            PIR; JS0609; JS0609
PROSITE; PS00903; C
                                                                                                                                                                                                                                                                                                                                  FAMILY
100
103
140 AA;
59 Z
100 Z
103 Z
: 15573 MW;
                                                                                                            CYT_DCMP_DEAMINASES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-46
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
; 12D8CAEC CRC32;
                                                                                                              1
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BSR\_BACCE Length: 140 February 14, 2000 08:02 Type: P Check: 8425

SEQUENCE

1 MKTFNISQQD LELVEVATEK ITMLYEDNKH HVGAAIRTKT GEIISAVHIE

51 AYIGRVTVCA EAIAIGSAVS NGQKDFDTIV AVRHPYSDEV DRSIRVVSPC

101 GMCRELISDY APDCFVLIEM NGKLVKTTIE ELIPLKYTRN

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_SEQUENCE 1.0

CADI_DICDI

STANDARD; PRT; 213 AA.

P54657;

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 35, Last sequence update)
01-ONV-1997 (Rel. 35, Last senotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
CALCIUM-DEPENDENT CELL ADHESION MOLECULE-1 (DDCAD-1) (GP24).
          SEQUENCE FROM N.A., AND SEQUENCE OF 43-62 AND 118-133.

SEQUENCE FROM N.A., AND SEQUENCE OF 43-62 AND 118-133.

WEDLINE; 96279194.

WONG E.F.S., BRAR S.K., SESAKI H., YANG C., SIU C.-H.;

WONG E.F.S., BRAR S.K., SESAKI H., YANG C., SIU C.-H.;

WOLCILL S., BRAR S.K., SESAKI H., YANG C., SIU C.-H.;

"MOLECULAR J. SECOLORIZATION OF DECEMBER OF THE SELECT OF THE PLASHALE OF THE PLASHALE OF THE PLASHALE MAY BE TRANSPORTED TO THE PLASHALE MEMBRANE VIA CONTRACTILE VACUOLES AND ITS CELL SURFACE ASSOCIATION MAY BE MEDIATED BY AN INTEGRAL MEMBRANE PROTEIN.

"I- DEVELOPMENTAL STAGE: EXPRESSED SOON AFTER THE INITIATION OF
                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota; Dictyosteliida; Dictyostelium
[]]
DEVELOPMENT
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IIAA_SEQUENCE 1.0

ICAMG_MOUSE
AC P49070;

AC P49070;

DT 01-FEB-1996 (R
CAMIG OR CAMI.
COC Eukaryota; Mete
OC Eukaryota; Mete
OC Eukaryota; Mete
OC Eukaryota; Mete
OC Eukaryota; Mete
RR SEQUENCE FROM
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RR SEQUENCE PROM
RR SEQUENCE 103-323--
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SEQUENCE
29
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SEQUENCE
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    Transmembrane.
TRANSMEM 188
TRANSMEM 239
SEQUENCE 294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-B6/CBA; TISSUE-THYMUS;
MEDLINE; 96011657.
KIM H.S., MORALES V.M., DASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus muscullus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      BLUMBERG R.S.;

Cloning of the gene encoding the mouse homologue of the calcium signal-modulating ligand.";

Gene 163:323-324(1995).

Gene 163:233-324(1995).

FUNCTION: LIKELY INVOLVED IN THE MOBILIZATION OF CALC
                                                                                                                                                                                                                                                                                             -i- FUNCTION: LIKELY INVOLVED IN THE MOBILIZATION OF CALCIUM AS A RESULT OF THE TCR/CD3 COMPLEX INTERACTION. BINDS TO CYCLOPHILIN B.-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                             EMBL; U21960; AAA87004.1;
MGD; MGI:104728; CAML.
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PTM: THE N-TERMINUS IS BLOCKED.
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SEGMENT AND 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      , MORALES V.M., DASS C.,
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255
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           POTENTIAL.
POTENTIAL.
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CA(2+)-BINDING
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           CRC32;
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CAMG_MOUSE
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                   EMBL; U18532; AAB59993.1; -
EMBL; X17430; -; NOT_ANNOTATED_CDS.
EMBL; X217430; -; NOT_ANNOTATED_CDS.
EMBL; D29177; AAA70045.1; -
EMBL; C291174; AAB505347.1; -
EMBL; Z99116; CAB14459.1; -
EMBL; Z99116; CAB14472.1; -
EMBL; Z99117; CAB14472.1; -
EMBL; Z9917; CAB1447; CAB147; CAB1447; CAB1447; CAB1447; CAB1447; CAB1447; CAB147; CAB1447; CAB1447; CAB147; CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOY-1990 (Rel. 16, Created)
01-NOY-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) (CDA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-168 / JH642;
STRAIN-168 / JH642;
KOBAYASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO
SATO T., TAKEUCHI M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SONG B.-H., NEUHARD J.; The property of the second of the second location, cloning and nucleotide sequence of the Bacillus subtilis cdd gene encoding cytidine/deoxycytidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-168
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METAL 53
METAL 86
METAL 89
SEQUENCE 136 AA;
                                                         CDSA_HAEIN
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STRAIN=BER;
MEDLINE; 93
THAM T.N.,
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CDSA_HAEIN STANDARD;
P44937; 032623; 032627;
01-NOV-1995 (Rel. 32, Cr
01-NOV-1995 (Rel. 32, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pirum.
Mycoplasma pirum:
Bacteria; Firmicutes; Bacillus/Clostridium
Mycoplasmataceae; Mycoplasma.
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P47718;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

01-FEB-1996 (Rel. 33, Last annotation update)

CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) (CDA).
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HSSP: P13652; 1AF2.
PROSITE: P800903; CYT_DCMP_DEAMINASES; 1.
Hydrolase; Zinc.
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PFAM; PF00383; dC
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133 AA;
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86 Z
89 Z
14854 MW;
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Last sequence update)
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ZINC (BY SIMILARITY).
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
; F377B762 CRC32;
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CDSA_HAEIN
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TRANSMEM 52
TRANSMEM 59
TRANSMEM 199
TRANSMEM 152
TRANSMEM 152
TRANSMEM 152
TRANSMEM 223
TRANSMEM 223
VARIANT 26
VARIANT 59
VARIANT 81
VARIANT 81
VARIANT 81
VARIANT 81
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EMBL; U60831; AAB61967.1;
EMBL; U60832; AAB61972.1;
TIGR: H10919; CDS; 1.
PROSITE; PS01315; CDS; 1.
PFAM: PF01148; Cyttd9tyltit
Transferase; Nucleotidylti
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STRAIN-RD / KW20;

MEDLINE; 95350630.

MEDLINE; 95350630.

MEDLICHNANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,

MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,

SCOTT J.D., SHRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,

WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,

UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,

UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,

GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,

VENTER J.C.;

VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLEIN M.H.;
Submitted (JUL-1997) to the EMBL/GenBar
Submitted (ACTIVITY: CTP + PHOSPHAIT
-!- CATALYTIC ACTIVITY: CTP + PHOSPHAIT
-:- CDP-DIACYLGLYCEROL.
-!- PATHWAY: PHOSPHOLIPID BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEME
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Last annotation update)
PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE
SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL
SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG
SYNTHASE).
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Bacteria; Pı
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Haemophilus influenzae
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  Length:
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52
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118
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288 AA;
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Nucleotidyltransferase;
pe; Inner membrane.
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AAB61967.1; -.
AAB61972.1; -.
     288
February
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                                              POTENTIAL.

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+ PHOSPHATIDATE =
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PYROPHOSPHATE
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OPLIREFVTT FLGVFIFLWL YTEGNYLDAG
ALLLVISYPK SAKFWSKNPL LQLLFAFSTL

RVFEQHLQLL LINAVSWWGL

MLKQRVLSAI VLIAAVLCAL

FLFTPFYFAL

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YFSGRAFGKR KLAPKVSPGK SWEGVIGGLI

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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
CORNEODESMOSIN (S P
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DOMAIN 155
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VELTEN F.W., ROGEL-GAILLARD C., RENARD C., PONTAROTTI P.,
TAZI-AHNINI R., VAIVAN M., CHARDON P.;
SUBMITTED JUN1997) to the EMBL/GenBank/DDBJ databases.
Submitted JUN1997) to the EMBL/GenBank/DDBJ IN CORNEODESMOSOMES;
-!- SUBCELLULAR LOCATION: SECRETED: FOUND IN CORNEODESMOSOMES;
INTERCELLULAR STRUCTURES THAT ARE INVOLVED IN DESQUAMATION
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its two mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-MAR-1992 (Rel. 21,
15-JUL-1999 (Rel. 38,
62_MITOTIC-SPECIFIC C
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SEQUENCE
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                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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itheria, Cetartiodactyla, Suina, Suidae, Sus
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 SEQUENCE FROM N.A
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arvota; Metazoa;
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21644 MW;
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36, Last sequence update)
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PROTEIN) (FRAGMENT).
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BUENO A., RICHARDSON H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch)
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PIR; A40316; A40316.
HSSP; P20248; 1JST.
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PROMITE; PS00292; CYCLINS; 1.

PRAM; PF00134; CYCLIN; 1.

CYCLIN; Cell Cycle; Cell division; Mitosis.

SEQUENCE 415 AA; 47827 MW; ED01A48C CRC32;
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CH19_DROGR
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P13427:
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CHORTON PROTEIN S19.
CP19 OR S19.
                   This SWISS-PROT entry is copyright. It is produced through a centre of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or or send an email to license@isb-sib.ch).
                                                                                                                                                          SEQUENCE FROM N.A.

MEDILNE; 88297142.

MARTINEZ CRUZADO J.C., SWIMMER C., FENERJIAN M.G., KAFATOS F.C.;

MARTINEZ CRUZADO J.C., SWIMMER C., FENERJIAN M.G., KAFATOS F.C.;

Tayolittion of the autosomal chorion locus in Drosophila. I. General repolitions of the locus and sequence comparisons of genes s15 and organization of the locus and sequence.

Sign in evolutionary distant species.";

Genetics 119:663-677(1988).
                                                                                                                                                                                                                                                                                           Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).
Bukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Bukaryota: Meoptera: Endopterygota; Diptera; Brachycera; Musc
Ephydroidea: Drosophilidae: Drosophila.
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B-type cyclin functioning early in
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                                            ID COAT_TCV
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STRAIN-2.4.1;
MEDLINE; 95238260.
SCHILKE B.A., DONOHUE T.J.;
"Chrk positively regulates transcription sphaeroides cytochrome c2 gene.";
J. Bacteriol. 177:1929-1937(1995).
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 01-JAN-1988 (Rel. 01-JAN-1988 (Rel.
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: POSITIVELY REGULATES TRANSCRIPTION OF THE CYCA GENE
FOR CYTOCHROME C2. MAY PLAY A ROLE IN THE INACTIVATION OF THE RPOE
GENE.
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
TRANSCRIPTIONAL ACTIVATOR CHRR.
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FLYBASE; FBgn0012320; Dgri\Cp19
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38 C -> R (IN CHR4 MUTANT;
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                                                                                                            DRFGAGDIEI
                                                                                                                                                               LSEGSLASVM
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                                                                                                                                      GGGVRQAILP
06, Created)
06, Last sec
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                                                                                                                                                             AQLDRQIQRP
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                                                                                                            AATDAPLREN
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sequence

ID COAT\_TOBSV

STANDARD

PRT;

237

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COAT_TCV
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CONFLICT
SEQUENCE
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HOGLE J.M., MAEDA A., HARRISON S.C.;
"Structure and assembly of turnip crinkle virus. I. X-ray crystallographic structure analysis at 3.2-A resolution.";
J. Mol. Biol. 191:625-638 (1986).
J. MOl. Biol. 191:625-638 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 87283926.
STOCKLEY P.G., MORRIS T.J.;
"Structure and assembly of turnip crinkle virus. IV. Analysis of the coat protein gene and implications of the subunit primary structure.";
                                                                                                                                                                                                                                                                                                      EMBL; X05193; CAA28823.1; -.
EMBL; M22445; AAA96971.1; -.
PIR; JA0111; VCVETC.
PIR; S07285; S07285.
HSSP; P11795; ZTEV.
PROSITE; D800555; ICOSAH_VIR_COAT_S; 1.
PROMSTE; P500729; Viral_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           viruses; ssRNA
                                                                        201
                                                                                                  151
                                                                                                                            101
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MEDLINE; 89243179.
CARRENGTON J.C., HEATON L.A., ZUIDEMA D., HILLMAN
"The genome structure of turnip crinkle virus.";
virology 170:219-225(1989).
351
                        301
                                                251
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COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Biol. 194:265-276(1987).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: COAT PROTEINS FROM CARMOVIRUSES (CARMV, MNSV, TCV), DIANTHOVIRUSES (RCMVV), SOBEMOVIRUSES (MCMV, SBMV), TOMBUSVIRUSES (AMCV, CNV, CYRSV, AND TBSV), AND TNV ARE RELATED IN THEIR S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGION
                                                                                                                                                                                                      Length: 351
                        ENADASDESV
                                                GDFAGVKDGP
                                                                                                                            PKYTTAVLNP
                                                                                                                                                                              MENDPRVRKF ASDGAQWAIK
                                                                                                                                                                                                                                                                                              protein.
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82
239
252
252
351 AA;
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                                                RLVSWSKTKG
                                                                                                    PPPNDLASLY
                                                                                                                           SEPGTFNQLI KEAAQYEKYR
                        LGEAAAGSVQ
                                                                        KLIMATYGQG
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238 S
351 P
252 D
38052 MW;
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                                                                                                    NIEGCVSSVP
                                                                                                                                                                             WOKKGWSTLT
                                                                                                                                                                                                     14, 2000 08:02 Type:
                        WAGVKVAERG
                                                TAGWEHDCHF
                                                                                                                                                      TOPRVSTARD
                                                                        ANDAAQLGEV
                                                                                                                                                                                                                                          R DOMAIN, INTERACTION WITH RNA
S DOMAIN, VIRION SHELL.
P DOMAIN, PROJECTING.
D -> Q (IN REF. 2).
                                                                                                                                                                                                                               -> Q (IN REF. 2).
064C2069 CRC32;
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                                                LGTGNFSLTL FYEKAPVSGI
                                                                                                                                                                              SROKOTARAA MGIKLSPVAC
                                                                                                                            FTSLRFRYSP
                                                                                                                                                      GITRSGSELI
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                        QGVKMVTTEE
                                                                                                    WIGFILIVPI
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                        QPKGKLQALF
                                                                                                    DSTDRFVADG
                                                                                                                                                      TTLKKNTDTE
                                                                        RTGSTSDAQI
                                                                                                                            MSPSTTGGKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outstation
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COAT_TOBSV Length: 237 February 14, 2000 08:02
RACE BERNELL B
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upda
21-JUL-1986 (Rel. 24, Last annotation up
01-DEC-1992 (Rel. 24, Last annotation up
COAT PROTEIN (P4 PROTEIN).
Tobacco streak virus (strain wC) (TSV).
Viruses; ssRNA positive-strand viruses,
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MEDLINE; 84169544.

CORNELISSEN B.J.C., JANSSEN H., ZUIDEMA D., BOL J.F.;

CORNELISSEN B.J.C., JANSSEN H., ZUIDEMA D., BOL J.F.;

CORNELISSEN B.J.C., JANSSEN H., ZUIDEMA D., BOL J.F.;

Nucleic Acids Res. 12:2427-2437(1984).
                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE: 97426617.
BLATTNER F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
GREGOR J., DAVIS N.W., KI
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P36562: P78075;
01.JUN-1994 (Rel. 29, Created)
01.JUN-1997 (Rel. 35, Last sequence update)
01.NOV-1997 (Rel. 35, Last sequence update)
15.DEC-1998 (Rel. 37, Last annotation update)
15.DEC-1998 (Rel. 37, Last annotation update)
NICOTINATE. VUCLEOTIDE-DIMETHYLEBRAZULE PHOSPHORIBOSYLTRANSFERASE).
(EC_2.4.2.21) (NN:DBI PRT) (N1-ALPHA-PHOSPHORIBOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X00435; CAA25133.1; -. PIR; A04206; VCBVWC. SEQUENCE 237 AA; 26237 MW
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STRAIR-K12 / W3110;
MEDLINE; 96062218.
LAWRENCE J.G., ROTH J.R.;
"The cobalamin (coenzyme B12) biosynthetic coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COBT_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
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                      SEQUENCE FROM N.A. STRAIN-K12;
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                                                                                                       complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                           T G. III, BLOCH C.A., PERNA N.T., BURLAND V., S J., GLASNER F.D., RODE C.K., MAYHEW G.F., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Enterobacteriaceae
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COBT_ECOLI
      ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T.,
ISONO K., KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M.,
AKKIO K., MIKI T., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K.,
NAKAMDE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T.,
SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H.,
TAKEBOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.;
TA 460-kb DAN sequence of the Escherichia coli K-12 genome
TA 460-kb DAN sequence of the Escherichia coli K-12 genome
COITESPONDING TO THE 40.1-50.0 min region on the linkage map.";
NA Res. 3:379-392(1996).
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SEQUENCE OF 1-188 FROM N.A.

SETALINE (12 / DH5-ALPER),

COLLINS C. M. , GUTMAN D.M. , ISAZA J.;

COLLINS C. M. , GUTMAN D.M. , ISAZA J.;

COLLINS C. M. , GUTMAN D.M. , ISAZA J.;

SUBMILTED (12 / N. )

FUNCTION: CATALYSES THE SYNTHESIS OF '5,6-DIMETRICIBENZIMIDAZOLE

(DMB), THE LOWER LIGAND OF B12 AND THE TRANSFER OF RIBOSE

(DMB), THE LOWER LIGAND OF B12 AND THE TRANSFER OF RIBOSE

(DMB), THE LOWER LIGAND OF B12 AND THE TRANSFER OF RIBOSE

(DMB), THE LOWER LIGAND OF B12 AND THE TRANSFER OF RIBOSE

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(DMB), THE LOWER LIGAND OF B12 AND THE LOW
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EMBL, AB000291; AAC75052.1;
EMBL, D90837; CAB21728.1; --
EMBL, D90838; CAB21739.1; --
EMBL, L25054; AAA56876.1; --
                                                                                                                              _SEQUENCE 1.0 STANDARD; PRT; 2
COX3_SCHCO STANDARD; PRT; 2
P14058;
01-JAN-1990 (Rel. 13, Created)
01-FEB-1999 (Rel. 33, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
CYTOCHROME C OXIDASE POLYPEPTIDE III (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycosyltransferase
CONFLICT 271
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Schizophyllum commune (Bracket fungus).
Mitochondrion.
Bukaryota; Fungi; Basidiomycota; Hymeno
Schizophyllaceae; Schizophyllum.
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n biosynthesis; Porphyrin biosynthesis; Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                              NMEMRLGEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                              VLLDGFLSYA
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301 L
36987 MW;
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-> V (IN REF. 1).
86515DE7 CRC32;
                                    Hymenomycetes;
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                                                                                                                                                                                             update)
                                                                                                                                          n update)
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                                                                                                                                                                                                                                                                         268
                                                                                                                                                                                                                                                                                                                                                                                                    AACAIYNNMG
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ID COX4_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COX3_SCHCO Length: 268
                                                                                                              KAWAMUKAI M.;

Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.

-!- SUBGUNIT: COMPOSED OF AT LEAST 11 SUBGUNITS.

-!- SUBGULLAR LOCATION: MITOCHONDRIAL INURE MEMBRANE.
-!- SUBGULLARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.

-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
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EMBL; AB000399; BAA19097.1;
                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
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                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
MEDLINE; 89106272.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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25E315EF CRC32;
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RT RAX
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                                                            (P36) (E30).

Plsum sativum (Garden pea).

Plsum sativum (Garden pea).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoid.
                                                                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, CHLOROPLAST PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                            Comp. bi-
                                                                                                                                                                                                                                     101 GIVTKDGNNL QLRA
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                     "Exoskeletal proteins from the crab, Comp. Biochem. Physiol. 0:0-0(1999).
-1- TISSUE SPECIFICITY: CALCIFIED SHE STRUCTURAL PROTEINS OF CUticle; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
CUTICLE PROTEIN CP1158 (CPCP1158)
Cancer pagurus (Rock crab).
Eukaryota, Metazoa, Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Cancroidea; Cancridae; Cancer.
                                                                                                                                                                                                                                                                51
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Oxidocreductase; MiTRANSIT 11
CHAIN 34
METRI 120
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METAL
SEQUENCE
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                                                                                                                                                                                                                                                    QAAAPAPPLP VSHYVASQQS VVGPSGIVSP SGNVQFSHEF ADNVVLVGPS
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                                                                                                                                                                                                                                                                                                                                114 AA;
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COX5B; 1.
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11601 MW;
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120
143
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PYRROLIDONE
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n; Transit peptide; Zinc.
MITOCHONDRION (BY SIMILARITY).
CYTOCHROME C OXIDASE POLYPEPTIDE
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                  SHELL.
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SEQUENCE FROM N.A., AND SEQUENCE STRAINSCV. PROGRESS NO: 9; TISSUE MEDILINE; 91035597.
SCHNELL D.J., BLOBEL G., PAIN D.;
"The chloroplast import receptor"

SEQUENCE OF 73-98; 9; TISSUE-SEEDLING,

249-260;

269-289

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324-350

Papilionoideae;

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STERE EREPERT TO SOLVE THE STERE TO SOLVE THE STERE THE 
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"Molecular cloning and structural analysis of the phosphate
translocator from pea chloroplasts and its comparison to the spinach
phosphate translocator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chloroplast e
J. Cell Biol.
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modified and this statement is not remov
entities requires a license agreement (S
or send an email to license@isb-sib.ch)
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DOMAIN
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PIR; S23774, S23774.
Transmembrane; Chloroplast; '
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DOMAIN
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FUNCTION: MEDIATES THE EXPORT OF FIXED CARBONS FROM THE
CHLOROPLASTS INTO THE CYTOSOL IN THE FORM OF TRIOSE PHOSPHATES.
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LOCATED IN
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. TOCATED
ZONES OF CONTACT BETWEEN THE INNER AND OUTER MEMBRANE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLOROPLAST.
SIMILARITY: STRONG, TO OTHER PLANTS CTPT. ALSO SIMILAR TO
YEAST PROTEIN SLY41.
CAUTION: WAS ORIGINALLY THOUGHT TO FUNCTION AS A CHLOROPLAST
PROTEIN IMPORT RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                MESRVLSRAT TLSSLPTLNK LHRLPLANAS LPSVKSFGSV SDGGNLVWGR
                                                                                                                                                                                                                                                              GFFFFTWYFL
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                                                                                                                                                                                                                  LPKRAPIDGN
                                           KRVFVIGFSI
                                                                                    GFNDAIAKVG
                                                                                                                                NISFTYRSIY
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l. 111:1825-1838(1990).
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                                                                                                                                                                                                                                                                                                            LKKGASLLRP
                                                                                    LVKFVSDLFW
                                                                                                                                SKKAMTDMDS
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                                                                                                                                                                                                                                                                                                              CPATAGGNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transit peptide; Transport. CHLOROPLAST. TRIOSE PHOSPHATE/PHOSPHATE
                                              TGIGTGIAIA
                                                                                         VGMFYHLYNQ
                                                                                                                                  TNIYAYISII
                                                                                                                                                                              SLAPVVIGVS
                                                                                                                                                                                                                       CHALGHVISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL:
INTERMEMBRANE SPACE (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC1E795 CRC32;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (SEP-1994)
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01-FEB-1994 (Rel. 28, Last sand
01-FEB-1994 (Rel. 28, Last and
CYTOCHROME AA3 CONTROLLING PRO
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Bacteria; Firmicutes; Bacillus/Clostridium group:
Bacillus/Staphylococcus group; Bacillus.
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  MEDLINE; 93107080.

QUIRK P.G., HICKS D.B., KRULWICH T.A.;

Cloning of the cta operon from alkaliphilic Bacillus characterization of the pH-regulated cytochrome caa3 o encodes.";
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FUNCTION: REPRESSOR FOR THE CSC OPERON. BINDS D-FRUCTOSE I
AN INDUCER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE LACI FAMILY OF TRANSCRIPTIONAL
DECITA PROFES
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1995 (Rel. 31, Last sequence update)
1998 (Rel. 37, Last annotation update)
0PERON REPRESSOR (CSC OPERON REGULATORY
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IIAA_SEQUENCE 1.0

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STRAIN-168;

BERTERO M., PRESECAN E., GLASER P., RICHOU A., DANCHIN A.;

SUBMITTED M., PRESECAN E., GLASER P., RICHOU A., DANCHIN A.;

SUBMITTED M., CAUGHOUT CONTROL OF CONTR
                                                         EMBL; M23915; AAA50254.1; --
EMBL; Z98682; CAB11340.1; --
EMBL; Z99111; CAB13360.1; --
PIR; A33960, A33960.
SUBTILIST; BG10213; CTAA.
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"Isolation and sequence of ctaA, a gene required for cytochrome biosynthesis and sporulation in Bacillus subtilis.";
J. Bacteriol. 171:4967-4978(1989).
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Bacteria; Firmicutes; Ba
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
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PIR; A45335; A45335.
Sporulation; Membrane.
SEQUENCE 297 AA; 32326 MW; BA198CC1 CRC32;
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-!- FUNCTION: CTAA IS REQUIRED FOR CYTOCHROME AA3 BIOSYNTHESIS AI INDEPENDENTLY FOR SPORULATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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us group; Bacillus.
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Membrane

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IPAA_SEQUENCE 1.0

ID CY2_RHOTE
AC P0098;
AC P0098;
DT 21-JUL-1986 (R
DT 21-JUL-1986 (R
DT 21-JUL-1995 (R
RT STRAIN=3761;
RX MEDLINE; 79199
RA AMBLER R.P., W
RT MADLER R.P., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIAA_SEQUENCE 1.0

ID CU04_BLACR
AC P80675;
DT 15-JUL-1998 (F
DT 1
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SEQUENCE.

SEQUENCE.

SEQUENCE.

STRAIN-3761;

MEDILINE, 79199668.

MEDILINE, 79199668.

MADDER R.P., MEYER T.E., KAMEN M.D.;

"Anomalies in anino acid sequences of small cytochromes c and cytochromes c from two species of purple photosynthetic bacteria.";

Nature 278:661-662(1979).

-I- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR, PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00098;
21-JUL-1986 (Rel. 0
21-JUL-1986 (Rel. 0
01-NOV-1995 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodocyclus tenuis (Rhodospirillum tenue).
Bacteria, Proteobacteria, beta subdivision, Rhodocyclus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 HAAISPLSVV SHPVVSPLVH VPQVVYV
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REPEAT 84
SEQUENCE 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cuticular proteins from the giant cockroach, Insect Biochem. Mol. Biol. 27:109-120(1997). Structural protein; Cuticle; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 97218697.
JENSEN U.G., ROTHMANN A., SKOU L., ANDERSEN S.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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EDLINE; 97218697.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01, Created)
01, Last sequence update)
32, Last annotation update)
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2.
www; 26A82D7C CRC32;
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01-AUG-1992 (Rel. 23, Last
01-NOV-1997 (Rel. 35, Last
CYN OPERON TRANSCRIPTIONAL
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92276346.

SUNG Y.-C., FUCHS J.A.;

"The Escherichia coli K-12 cyn opmember of the lysk family.";

J. Bacteriol. 174:3645-3650(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
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MEDLINE: 97426617.

BLATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.

BLATINER F.R., PLUNKETT G. III, BLOCH C.A., RODE C.K., MAYHEW G.F.,

BILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,

GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,

MAU B., SHAO Y.;

MAU B., SHAO Y.;
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          The complete genome sequence of Escherichia science 277:1453-1474(1997).
  EMBL; M93053; AAA23628.1; -
EMBL; AE000141; AAC734441.1;
EMBL; U73857; AAB18062.1; AI
PIR; A41900; A41900.
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STRAIN-K12 / MG1655;
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SIMILARITY: THIS SEQUENCE IS MORE CLOSELY RELATED TO THE SEQUENCE
OF CYTOCHROME C551 FROM PSEUDOMONAS AND AZOTOBACTER THAN TO THE
SEQUENCES OF CYTOCHROME C2 FROM OTHER SPECIES OF RHODOSPIRILLUM.
1, A00090; CCCP2T.
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HEME (COVALENT).
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IRON (HEME AXIAL LIGAND).
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S73C3CFO CRC32;
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P SEQUENCE OF 30-85, AND ACTIVE SITE.

P SEQUENCE OF 30-85, AND ACTIVE SITE.

P MEDLINE, 89350853

X LEYH-BOUILLE M., VAN BEBUMEN J., RENIER-PIRLOT S., JORIS B.,

LEYH-BOUILLE M., VAN BEBUMEN J.-M.;

A NGUYEN-DISTECHE M., GHUYSEN J.-M.;

The Streptomyces KL5 DD-Peptidase/penicillin-binding protein. Active

"The Streptomyces KL5 DD-ALANINE C-TERMINAL D-ALANINE STREPTOMYCES PENICE

"The Streptomyces KL5 DD-ALANINE CABBOXYEPTIDASE FROMYCES

"The Streptomyces From Streptomyces From Streptomyces From Streptomyces

"The Streptomyces From Streptomyces From 
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PROSITE; PS00044; HTH_LYSR_FAMILY:
PFAM; PF00126; HTH_l; 1.

Transcription regulation; DNA-bindi
TRANSCRIPTION 18
37
H-T-H
DNA_BIND
18
37
SEQUENCE 299 AA; 32961 MW; 0A83
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01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
D-ALANYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR
PEPTIDASE) (DD-CARBOXYPEPTIDASE).
Streptomyces sp. (Strain K15).
Streptomyces sp. (Strain K15).
Streptomyces sp. (Strain K15).
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DACX_STRSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALOMEQUE MESSIA P. ENGLEBERT S., LEYH-BOUILLE M., PALOMEOUE MESSIA DUEZ C., HOUBA S., DIDEDERG O., VAN BEEUMEN J., GHUYSEN J.-M.;

VAN BEEUMEN J., GHUYSEN J.-M.;

"Amino acid sequence of the penicillin-binding protein/DD-peptidase of streptomyces K15. Predicted secondary structures of the low Mr penicillin-binding proteins of Class A.";

penicillin-binding proteins of Class A.";

Biochem. J. 279:223-230(1991).
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                                                                        EMBL; X59965; CAA42591.1; -.
PIR; S04638; S04638.
PIR; S17674; S17674.
PFAM; PF00768; Peptidase_S11;
Hydrolase; Carboxypeptidase; I
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291
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H-T-H MOTIF (BY SIM
MW; 0A8298D6 CRC32;
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           D-ALANYL-D-ALANINE
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Streptomycetaceae; Streptomyces
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                   CARBOXYPEPTIDASE
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or send an enum.

R EMBL; U28135; AAB01679.1; .

JR EMBL; Z74954; CAA99237.1; .

JR EMBL; Z74955; CAA99239.1; .

DR EMBL; Z74955; CAA99239.1; .

DR PIR; D384848; D34848

BGD; L0003292; DBP5

DR PROSITE; PS00039; DEPAD; ATP_HELICASE; 1.

DR PFAM; PF00271; helicase_C; 1.

RW Helicase; ATP-binding; RNA-binding; Nuclear protein.

RW Helicase; ATP-binding; RNA-Dinding; Nuclear protein.

RW Helicase; ATP-binding; RNA-DINDING; Nuclear protein.

RW Helicase; ATP-binding; RNA-DINDING; Nuclear protein.

RW Helicase; ATP-BIND 138 145

ATP (POTENTIAL).

DEAD BOX.

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                                                                               !!AA_SEQUENCE 1.0
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SEQUENCE OF 237-425 FROM N.A.

MEDILINE; 90160368.

CHANG T.-H., AREMAS J., ABELSON J.;

"Identification of five putative yeast RNA helicase genes.";

Proc. Natl. Acad. Sci. U.S.A. 87:1571-1575 (1990).

-I- SUBCELULAR LOCATION. NUCLEAR (PROBABLE).

-I- SUBCELULAR LOCATION. NUCLEAR (PROBABLE).

-I- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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LANDT O., HIESEL R., UNSELD M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DBP5_YEAST STANDARD: PRT: 482 AA.
P20449;
01-FEB-1991 (Rel. 17, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROBABLE ATP-DEPENDENT RNA HELICASE DBP5 (HELICASE CA5/6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
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SOHN C., BOLOTIN-FUKUHARA M., DAIGNAN-FORNIER B., DANG D.V.,
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CONFLICT
CONFLICT
SEQUENCE
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70
83
291 AA;
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30257 MW;
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T -> Q (IN REF. 2).

D -> S (IN REF. 2).

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i HAA\_SEQUENCE 1.0
ID \_HAT\_CITER STANDARD,
AC \_ P455.13;
DT 01-NOV-1995 (Rel. 32, Created)

101

DNIVTSVALA

51

VLSKNPVYSN VMKEDDPQVI NHIALAKQAD LFLLPPASAN TLAHLAHGFA

LSHQLTKLGY HVNVFMTNAA KQFIPPLTLQ

Check: 9135

LPLEVPKFFA PAMNTKMYEN PITQSNITLL KKFGY

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MTKKILLAVS GSIAAYKAAD

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                                                                        Flavoprotein.

NON_TER 1

NON_TER 145

SEQUENCE 145 AA;
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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     GUTIERREZ J.A., CROWLEY P.J., BROWN D.P., HILLMAN J.D.,
YOUNGMAN P., BLEIWEIS A.S.,
"Insertional mutagenesis and recovery of interrupted genes of
Streptococcus mutans by using transposon Tn917: preliminary
Characterization of mutants displaying acid sensitivity and
J. Bacteriol 178:4166-4175(1996).

1- FUNCTION: FLAVORROTEIN AFFECTING SYNTHESIS OF DNA AND PANTOTHENATE
METABOLISM (BY SIMILARITY).
                                                                                                                                                                                                EMBL; U48885; AAC44502.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG (FRAGMENT).
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Length: 145 February 14, 2000 08:02 Type: P
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; 15819 MW;
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                                                                     24E84944 CRC32;
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DHAT_CITFR Length:
                                                          AA_SEQUENCE 1.0

DHAT KLEPN

O59477;

O1-NOV-1997 (Rel. 35, Created)

O1-NOV-1997 (Rel. 35, Last sequence upda

O1-NOV-1997 (Rel. 35, Last annotation upda)

O1-NOV-1997 (Rel. 35, Last annotation upda)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
1,3-PROPANEDIOL DEHYDROGENASE (EC 1.1.1.202) (3-HYDROXYPROPIONALDEHYDE
REDUCTASE) (1,3-PROPANEDIOL OXIDOREDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILIR: 9543488.

DANIEL R. BORNIGK R., GOTTSCHALK G.;
PURITICACTION of 1,3-propanediol dehydrogenase from Citrobacter Puritication of the green corresponding gene in Escherichia coll.";

1. Bacteriol 177:2151-2156(1995).

1. Bacteriol 177:2151-2156(1995).

1. Bacteriol GROUPS SEPARATED BY ONE OR TWO CARBON ATOMS. IN THE ALCOHOL GROUPS SEPARATED BY ONE OR TWO CARBON TOWNS. IN THE PREFERED PHYSIOLOGICAL DIRECTION, 3-HYDROXYPROPIONALDEHYDE IS THE PREFERED SUBSTRATE.

SUBSTRATE.

--- CATALYTIC ACTIVITY: PROPANE-1,3-DIOL + NAD(+) = 3-HYDROXYPROPANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Citrobacter freundii.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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MEDLINE; 95238288.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: U09771; AAB488481: 1. PROSITE; PS00913; ADH_IRON_1; 1. PROSITE; PS00060; ADH_IRON_2; 1. PRAM; PF00465; Fe-ADH; 1. PRAM; PF00465; Fe-ADH; 1.
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                                Klebsiella
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SIMILARITY: BELONGS TO THE
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                                                                                                                                                                                                                                   PEKFADIAEF
                                                                                                                                                                                                                                                                  SLLAGMAFNN
                   Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 AA;
                                  pneumoniae
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                                                                                                                                                                                                                                                                                                                               TKVKFVIVSW
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41481 MW; BAC88846 CRC32;
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                     gamma
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                                                                 sequence update)
annotation update)
ass (EC 1.1.1.202) (
L OXIDOREDUCTASE).
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                                                                                                                                                                                                           PRKGNEKEIA
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                       subdivision;
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                         Enterobacteriaceae.
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                                                                                                                                                                                                                                                                                                                                                                                                   EHCDIIVTVG
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DHAT_KLEPN Length:
SEQUENCE FROM N.A.
STRAIN-ATCC 25955;
STRAIN F.A., WILLARD B.L., CAMERON D.C.;
SKRALY F.A., WILLARD B.L., CAMERON D.C.;
SUBMITTED (NOV-1995) to the EMBL/GenBank/DDBJ data submitted (NOV-1995) to the EMBL/GenBank-DJG (NOV-1995) to the EMBL/GENBAR (NOV-1995) to the EMBL/
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SEQUENCE FROM
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PROSITE; PS00913; ADH_IRON_2; 1.
PROSITE; P$00060; ADH_IRON_2; 1.
PFAM; PF00465; Fe_ADH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _SEQUENCE 1.0
DHB3_HUMAN
P37058;
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VARIANT MPH TRP-80.

WEDLINE; 98429412.

BILBAO JR., LORIDAN L., A
BILBAO JR., LORIDAN L., A
novel missense (R80W) m
dehydrogenase type 3 gene
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                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ESTRADICL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (
TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE)
HSD1783 OR EDH1783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351
                                                                                                                                                                                                                  TISSUE=TESTIS; /
MEDLINE; 94355972.
GEISSLER W.M., DAV
MENDONCA B.B., ELL!
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                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANTS MPH Q-80; V-203;
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                                                                                                                                                       Male pseudohermaphroditism causeo
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SUBUNIT: HOMOOCTAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IRON-CONTAINING
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enet. 7:34-39(1994).
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                                                                                                                                                                                                                       DAVIS D.L., WU ELLISTON K.O.,
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     AUDI L., GONZALO E., CASTANO L.;
mutation in 17-beta-hydroxysteroi
e associated with male
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RUSSELL D.W
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D(+) = 3-HYDROXYPROPANAL
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gene

pseudohermaphroditism.";
Eur. J. Endocrinol. 139:330-333(1998).
1. FUNCTION: FAVORS THE REDUCTION OF ANDROSTENEDIONE TO TESTOSTERONE.
1. FUNCTION: FAVORS THE THE OTHERS EDH1/B ENZYMES USE NADH.
1. CATALYTIC ACTIVITY: ESTRADIOL-17-BETA + NADP(+) = ESTRONE +

NADPH.

PATHWAY: LAST ENZYME OF THE TESTOSTERONE BIOSYNTHESIS.

DISEASS: DEFECTS IN EDH17B3 GIVE RISE TO MALE PSEUDOHERWAPHRODISM (MPH). THESE 46,XY INDIVIDUALS HAVE UNAMBIGUOUS EMALE EXTERNAL GENITALIA AT BIRTH, BUT FALL TO MENSTRUATE AT THE TIME OF EXPECTED PUBERTY AND INSTEAD VIRILISE AS EVIDENCED BY GROWTH OF THE PHALLUS. BREAST DEVELOPMENT MAY OR MAY NOT TAKE PLACE.

SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR). 17-BETA-HSD 3 SUBFAMILY.

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P70385;
1 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 01-NOV-1997 (Rel. 37, Last sequence update)
T 15-DEC-1998 (Rel. 37, Last annotation update)
E ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BET)
E (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE)
SN HSD17B3 OR EDH17B3.
NS MUS musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Man
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                          ID DHB3_MOUSE
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biosynthesis; Oxidoreductase; NADP; Multigene
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R > V (IN MPH) /FTId=VAR_006954.
A -> V (IN MPH) /FTId=VAR_006955.
S -> L (IN MPH) /FTId=VAR_006956.
M -> V (IN MPH) /FTId=VAR_006957.
/FTId=VAR_006957.
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301 251 201 151 101

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CGCLAHEIIA

IILNRIPSRI

FYSSTAQRFL LTRYSDYLKR

TQLVLKHMES

RRKGLILNIS

SGAALRPWPL

YSLYSASKAF SSSGESQNLI TTGSGVKIVQ

EYRDKGIIIQ VLTPYSISTP MTKYLNNKMT KTADEFVKES

51

GAGDGIGKAY SFELARHGLN VVLISRTLEK LQTIAEEIER

HIKEHLEGLE NGILVNNVGM LPSFFPSHFL

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DHB3_MOUSE Length: 305 February 14, 2000 08:02 Type: P
                                                                            PFAM; PFO
Steroid b
NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                EMBL; U668
MGD; MGI:1
PROSITE; P
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch)
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MEDLINE; 97325842.

SHA J.A., DUDLEY K., RAJAPAKSHA W.R.A., O'SHAUGHNESSY P.J.;

"Sequence of mouse 17beta-hydroxysteroid dehydrogenase type 3 cDNA
"Sequence of incluse 17beta-hydroxysteroid dehydrogenase type 3 cDNA
and tissue distribution of the type 1 and type 3 isoform mRNAs.";

J. Steroid Biochem. Mol. Biol. 60:19-24(1997).

J. Steroid Biochem. Mol. Biol. 60:19-24(1997).

USES NADPH WHILE THE TWO OTHERS EDH17B ENZYMES USE NADH (BY
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                                                                                                                                                                                                                                                                                                                  SIMILARITY).

SIMILARITY: ESTRADIOL-17-BETA + NADP(+) = ESTRONE + NADPH

NADPH

PATHWAY: LAST ENZYME OF THE TESTOSTERONE BIOSYNTHESIS,

SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

FAMILY (SDR). 17-BETA-HSD 3 SUBFAMILY.
         MEKLFIAAGL FVGLVCLVKC
                                                                                                                   TE; PS00061; ADH_SHORT; 1.
PF00106; adh_short; 1.
id biosynthesis; Oxidoreduc
                                                                                                                                                                              U66827; AAB06793.1; -.
MGI:107177; HSD17B3.
                                                                            194
305 AA;
                                                                ils; Oxidoreductase; NADP; Multigene
73 NADP (BY SIMILARITY).
194
BY SIMILARITY.
34271 MW; 10CB2855 CRC32;
MRFSQHLFLR FCKALPSSFL RSMGQWAVIT
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ID DHB3_RAT
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
17-DEC-1998 (Rel. 37, Last annotation update)
18-DEC-1998 (Rel. 37, Last annotation update)
18-DEC-1998 (Rel. 37, Last sequence update)
18-DEC-1998 (Rel. 37, L
                                                                                                           ---
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

KHANUM A., TSAI-MORRIS C.-H., DUFAU M.L.;

SUBMILTED (NOV-1997) to the EMBL/GenBank/DDBJ databases.

'I FUNCTION: FAVORS THE REDUCTION OF ANDROSTENEDIONE TO TES

USES NADEH WHILE THE TWO OTHERS EDH17B ENZYMES USE NADH

SIMILARITY).

'I CATALYTIC ACTIVITY: ESTRADIOL-17-BETA + NADP(+) = ESTRON
PATHWAY: LAST ENZYME OF THE SIMILARITY: BELONGS TO THE SFAMILY (SDR). 17-BETA-HSD 3
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                                                                               THE TESTOSTERONE
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                                                         DEHYDROGENASES/REDUCTASES
                                                                                                                          BIOSYNTHESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
Rattus.
                                                                                                                                                                                                                                                    ESTRONE
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DHB3_RAT
                                                                                                           !!AA_SEQUENCE 1.0
ID DHBK_MOUSE
                                                         DHBK_MOUSE
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15-DEC-1998 (Rel. 38, Last annotation
15-JUL-1999 (Rel. 38, Last annotation
putATIVE STEROID DEHYDROGENASE KIK-I o
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collable through the swiss institute of Bioinformatics and the swiss outstands the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institute. There are no restrictions in use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. However, is a substitution of the statement is not removed. The substitution is not remov
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-1996) to The SHORT CHAIN DEHYDROGENASES/REDUCTASES
-!- SIMILARITY: BELONGS TO THE SHORT CHAIN DEHYDROGENASES/REDUCTASES
-!- SIMILARITY: BELONGS TO THE SHORT CHAIN DEHYDROGENASES/REDUCTASES
-!- SIMILARITY: BELONGS TO THE SHORT CHAIN DEHYDROGENASES/REDUCTASES
-!- SIMILARITY: SDR) 17-BETA-HSD 3 SUBFAMILY.
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STRAIN-BALB/C; TIS
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Eutheria; Rodentia;
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ACT_SITI
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                                                                                                                                                                                                                                            PFAM; PF00106;
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AF035156; AAB99739.1; FALSE_NEG.
(ITE; PS00061; ADL_SHORT; FALSE_NEG.
) PF00106; adh_Short; 1

Old blosynthesis; Oxidoreductase; NADP; Multig
Old blosynthesis; Oxidoreductase; NADP (BY SIMILARITY)

JIND 194 194 BY SIMILARITY

AP723 MW; BFB8CBB9 CRC32;
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MECAPPAAGE LYWVGASTIA YLALRASYSL FRAFQVWCVG NEALVGPRLG
                                                            Length: 312
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FOOLOG: add, short; 1.

FOOLOG: add, short; 1.

FOOLOG: NADP; Multigene family.
biosynthesis; Oxidoreductase; NADP; Multigene family.
B 75 79 NADP (BY SIMILARITY).
B 202 202
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B 202 202
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B 312 AA; 34742 MW; 121C2554 CRC32;
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                                                                    February 14, 2000 08:02
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GIGKAYAEEL

AKRGMKIVLI SRSQDKLNQV SNNIKEKFNV

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Homo sapiens (Human)
Eukaryota; Metazoa; (
Eutheria; Primates;

Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.

Mammalia

||IAA\_SEQUENCE 1.0 ID DHC3\_HUMAN AC 075828; DT 15-DEC-1998 () DT 15-DEC-1999 () DT 15-DEC-1999 () DE CARBONYL REDU DE CARBONYL REDU DE REDUCTASE 3). GN CER3. GN CER3. GN CER3. GE Eukaryota; Me OC Eutheria; Pri

REDUCTASE 3).

301

RARFLKKKMK

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0.75828; 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1999 (Rel. 39, Last annotation update) CARBONYL REDUCTASE [NADPH] 3 (EC 1.1.1.184) (

(NADPH-DEPENDENT CARBONYL

STANDARD;

PRT;

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!!AA_SEQUENCE 1.0
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O57314;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
pUTATIVE STEROID DEHYDROGENASE SPM2 (EC 1.1.1.-).
Anas platyrhynchos (Domestic duck).
Lakaryota; Metazoa; Chordata; Craniata; Vertebrata;
pukaryota; Metazoa; Chordata; Craniata; Anas.
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                                                                                                                                                                                                                                       EMBL; AB009304; BAA23765.1; -. PROSITE; PS00061; ADH_SHORT; 1. PFAM; PF00106; adh_short; 1.
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ACT_SITE
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                                                                                                                                  MIPAAGILWW VGALGALYAA VRGALGLIGA LRVWGIGAGR AALGPGIGAW
                                                                                KVIVADFGER
PETYVRAAIG TVGLQSQTNG
                             YSASKAFVDY FSRGLHAEYK
                                                                                                                                                           Length: 312
                                                                                                                                                                                    biosynthesis; Oxidoreductase; NADP; Multigene family.

48 77 NADP (BY SIMILARITY)

E 201 201 BY SIMILARITY.

E 312 AA; 33896 MW; 3DDB3A6D CRC32;
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                                                        IMSVCKMTRL
                                                                                  EDIYDRIRAG
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       CLPHAFMGWV FSILPTSTVM NLLMKTNKQJ
                                SKGIIVQSVM
                                                         VLPGMLERSK GVILNISSAA GMYPTPLLTL
                                                                                     LEGLEIGVLV
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                                        ISKPSFDKPT
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IIAA_SEQUENCE 1
ID DHCA_HUWAN
AC P16152;
DT 01-APR-199
DT 15-DEC-199
DE CARBONYL R
ERDUCTASE
DE (PROSTAGLA
DE (NADP+)) (
GN CBR1 OR CB
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INIT_MET 0 0
NP_BIND 9 33
ACT_SITE 193 193
SEQUENCE 276 AA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHCA_HUMAN STANDARD; PRT; 276 AA.
P16152;
01-APR-1990 (Rel. 14, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CARBONYL REDUCTASE (NADPH) 1 (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL REDUCTASE 1) (PROSTAGLANDIN-EZ 9-REDUCTASE) (EC 1.1.1.189)
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EMBL; AB003151; BAA34207.1;
MIM; 603608; -
PROSITE; PS00061; ADH_SHORT;
PFAM; PF00106; adh_short; 1.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 98414514.
WATANABE K., SUGAWARA C., ONO A., FUKUZUMI Y., ITAKURA S.,
WAMAZAKI M., TASHIRO H., OSOGGAWA K., SOEDA E., NOMURA T.;
YAMAZAKI M., TASHIRO H., OSOGGAWA K., SOEDA E., NOMURA T.;
"Mapping of a novel human carbonyl reductase, CBR3, and ribosomal
pseudogenes to human chromosome 21q22.2.";
Genomics 52:95-100(1998).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
                                                                                                             GABBAY K.H.;
"Human carbonyl reductase. Nucleotide sequence analysis of a cDNA amino acid sequence of the encoded protein.";
J. Biol. Chem. 263:16185-16188(1988).
                                                                                                                                                                                            WERMUTH B., BOHREN K.M., GABBAY K.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROSTAGLANDIN 9-KETOREDUCTASE) (15-HYDROXYEROSTAGLANDIN DEHYDROGENASE [NADP+]) (EC 1.1.1.97).
CBR1 OR CBR OR CRN.
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                                                      SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
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                                                            AND
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                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE
                                                            PARTIAL SEQUENCE
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NADP (BY SIMILARITY).
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; AE7D716B CRC32;
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                                                                                                                                           DHCA_HUMAN
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Oxidoreductase; NADP; Acetylation.
INIT_MET 0 0 ACETYLA
MOD_RES 1 1 1 ACETYLA
MOD_RES 238 238 N6-(1-C
NP_BIND 9 33 NADP (B
ACT_SITE 193 193 BY SIMI
SEQUENCE 276 AA; 30244 MW; 470A0
                                                                                                                                PIR; A31912; RDHUCB.
PIR; S09013; S09013.
HSSP; P14061; 1EDW.
MIM; 114830; -.
PROSITE: P800061; ADH_SHORT; 1
PFAM; PF00106; adh_short; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KROOK M., GHOSH D., STROEMBERG R., CARLQUIST M., JOERNVALL H.:

"Carboxyethyllysine in a protein: native carbonyl reductase/NADP(+)-
dependent prostaglandin dehydrogenase.";

Proc. Natl. Acad. Sci. U.S. A. 90:502-506(1993).

-!- FUNCTION: CATALYZE THE REDUCTION OF A WIDE VARIETY OF CARBONYL
COMPOUNDS INCLUDING THE ANTIHUMOR ANTHRACYCLINE ANTIBIOTICS.

-!- COMPOUNDS INCLUDING THE ANTIHUMOR ANTHRACYCLINE ANTIBIOTICS.

-!- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.

-!- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9,11,15-TRIHYDROXY-9-OXOPROSTA-
5,13-DIENOATE + NADPH.

5,13-DIENOATE + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE; 98414514.

WATANABE K., SUGAWARA C., ONO A., FUKUZUMI Y., ITAKURA S.,

WATANABE M., SUGAWARA C., ONO A., FUKUZUMI Y., ITAKURA S.,

"YAMAZAKI M., TASHIRO H., OSOEGAWA K., SOEDA E., NOMURA T.;

"Mapping of a novel human carbonyl reductase, CBR3, and ri)

pseudogenes to human chromosome 21q22.2.";

Genomics 52:95-100(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORREST G.L., AKMAN S., KRUTZIK S., PAXTON R.J., SPARKES R.S., DOROSHOW J., FELSTED R.L., MOHANDAS T., BACHUR N.R.;
"Induction of a human carbonyl reductase gene located on chromosome 21.";
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               EMBL; J04056; AAA52070.1; -. EMBL; M62420; AAA17881.1; -. EMBL; AB003151; BAA33498.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92017676.

FORREST G.L., AKMAN S., DOROSHOW J., RIVERA H., KAPLAN W.D.;

"Genomic sequence and expression of a cloned human carbonyl reductase gene with daunorubicin reductase activity.";

Mol. Pharmacol. 40:502-507(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,13-DIENOATE + NADPH.

CAPALYTIC ACTIVITY: (52,13E)-(15S)-11-ALPHA,15-DIHYDROXY-9-OXOPROST-13-ENOATE + NADP(+) = (52,13E)-11-ALPHA-HYDROXY-9,15-DIOXOPROST-13-ENOATE + NADPH.
SUBUNIT: MONOMER.
SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
92017676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND POST-TRANSLATIONAL MODIFICATIONS
ACETYLATION.
N6-(1-CARBOXYETHYL).
NADP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
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51 ш

> SSGIHVALVT Length: 276

GGNKGIGLAI

VRDLCRLFSG DVVLTARDVT RGQAAVQQLQ

February

14, 2000

08:02

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Check:

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AEGLSPREHQ LDIDDLQSIR ALRDFLRKEY GGLDVLVNNA GIAFKVADPT

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TO DI 
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A_SEQUENCE 1.0
DHCA_RABIT
P47844;
01-FEB-1996 (
01-FEB-1996 (
15-DEC-1998 (
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DHCA_MOUS
P48758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U31966; AAB1900b.1; -.
MGD; MGI:88284; CBR. CBR. SHORT; 1.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_short; 1.
Oxidoreductase; NADP; Acetylatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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MOD_RES
NP_BIND
ACT_SITE
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-!- CATALYTIC ACTIVITY: R-CHOH-R' +
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Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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01-FEB-1996 (Rel. 33, Last seq
15-JUL-1998 (Rel. 36, Last ann
CARBONYL REDUCTASE [NADPH] (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEI J., DLOUHY S.R., HARA A., GHETTI B., HODES M.E.;
"Cloning a cDNA for carbonyl reductase (Cbr) from mouse cerebellum:
murine genes that express cbr map to chromosomes 16 and 11.";
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SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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     33,
37,
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p; Acetylation.

0 BY SIMILARITY.

1 ACETYLATION (BY SIMILARITY).

13 NADP (BY SIMILARITY).

193 BY SIMILARITY.

193 BY SIMILARITY.

30597 MW; 09438E74 CRC32;
Created)
Last sequence update)
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annotation update)
(EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL
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Mus.
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MEDLINE; 95197021.
GONZALES B., SAPRA A., RI
"Cloning and expression c
reductase.",
Gene 154.297-298(1995).
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                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Lágomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBONYL REDUCTASE [NADPH] (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  RIVERA H., K
n of the cDNA
                                                                                                                                                                                                                                                                                                                               KAPLAN W.D., YAM
NA encoding rabbit
                                                                                                                                                                                                                                                                                                                                  B., FORREST G.L.;
t liver carbonyl
                                                                                                                                                                                             collaboration -
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DHCA\_RABIT INIT\_MET
NP\_BIND
ACT\_SITE
VARIANT EMBL; U07051; AAA77670.1; -... EMBL; U09244; AAA82159.1; -... PROSITE; P800061; ADH\_SHORT; 1. PFAM; PF00106; adh\_Short; 1. Oxidoreductase; NADP. SEQUENCE Length: 276 214 276 AA; February 14, 2000 BY SIMILARITY.
NADP (BY SIMILARITY).
BY SIMILARITY
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A -> E (IN CLONE RCBR6;
V -> A (IN CLONE RCBR6;
V -> A (IN CLONE RCBR6;
H -> Q (IN CLONE RCBR6;
EAF9ZE81 CRC32; 08:02 Type: P RCBR6). RCBR6). RCBR6). Check:

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REGION COCO
                                                                                                            _SEQUENCE
DHCA_RAT
P47727;
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                  Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
Eutheria; Rodentia; Sci
                                                                    01-FEB-1996 (Rel. 3
01-FEB-1996 (Rel. 3
01-OCT-1996 (Rel. 3
CARBONYL REDUCTASE
                                                           REDUCTASE).
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                                                                                                                                                   VYLALLPPDA
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                                                                33, Created)
33, Last sequence update)
34, Last annotation update)
5 [NADPH] (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL
                 Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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                  Mammalia;
Rattus.
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SEQUENCE FROM

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DHCA_RAT
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TO NOD_RES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-COT-1996 (Rel. 34, Last annotation update)
01-COT-1996 (Rel. 34, Last annotation update)
GRANATICIN POLYKETIDE SYNTHASE PUTATIVE KETOACYL
                                                                                                                                                                                                                                 "Structure and deduced function opolyketide synthase gene cluster Tu22.";
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=TU22;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 1.3.1.-) (ORF5).
Streptomyces violaceoruber.
Bacteria; Firmicutes; Actir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Cloning and exp
Eur. J. Biochem
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MEDLINE; 95220378.
WERMUTH B., MAEDER-HEIN
                                                                                                                                                                                                                                                                                                        MEDLINE; 90060034.
SHERMAN D.H., MALPARTIDA F.,
HOPWOOD D.A.;
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by non
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SUBUNIT: MONOMER (BY SIMILARITY)
SUBCELULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
                                                                                                                   OJ. 8:2717-2725(1989).
PATHWAY: BIOSYNTHESIS OF THE POLYKETIDE ANTIBIOTIC GRANATICIN.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
                             SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the Ek
European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYLALLPPGA
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hem. 228:473-479(1995)
C ACTIVITY: R-CHOH-R'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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(P; Acetylation.

BY SIMILARITY.

1 ACETYLATION (BY SIMILARITY).

3 NADP (BY SIMILARITY).

193 BY SIMILARITY.

193 BY SIMILARITY.

30447 MW; D9BC158B CRC32;
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Institute. In
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EMBL outstation -
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IIAA_SEQUENCE I DEFRESTANTA C P41177; AC P411777; AC P41177; AC P41177; AC P41177; AC P41177; AC P41177; AC P4
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EMBL; Z11511; CAA77599.1; -.

PIR; S25079; S25079; S25079;
HSSP; P19992; 2HSD.

PROSITE; PS00061; ADH_SHORT; 1.

PFAM; PF00106; adh_Short; 1.

PFAM; PF00678; adh_Short; C2; 1.

Antibiotic biosynthesis; Oxidoreductase; NAD.

AND_BIND 10 34 NAD (BY SIMILARITY)

ACT_SITE 157 157 BY SIMILARITY.

SEQUENCE 261 AA; 27080 MW; 12DFE5B3 CRC32;
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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PFAM; PF00678; adh_short; C2; 1.

PFAM; PF00678; adh_short; C2; 1.

AntibLotic biosynthesis; Oxidoreductase; NAD.

NP_BIND 15 16 NAD (BY SIMILARITY).

ROT_SITE 168 BY SIMILARITY.

SEQUENCE 272 AA; 28393 MW; 1C3C79A3 CRC32;
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ARROWSMITH T.J., M
ROBINSON J.A.;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
00-CCT-1996 (Rel. 34, Last annotation update)
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EMBL; X16144; CAA34263.1; -.
PIR; S05397; S05397;
HSSP; P03617; 11FK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes from the monensin producer Streptomyces cinnamonensis.";
MO1. Gen. Genet. 234:254-264(1992).
-i- PARHWAY: BIOSYNTHESIS OF THE POLYKETIDE ANTIBIOTIC MONENCIN.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces cinnamonensis. Bacteria; Firmicutes; Actin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterisation of actI-homologous DNA encoding polyketide synthase genes from the monensin producer Streptomyces cinnamonensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261
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IIAA_SEQUENCE:

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Ol-FEB-1995 (Rel. 34, Las
Ol-OCT-1996 (Rel. 34, Las
DLTE PROTEIN.
DLTE OR IPA-IR.
Bacillus subtilis.
Bacteria; Firmicutes; Bac
Bacillus/Staphylococcus 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLASER P. KUNST F. ARNAUD M., COUDART M.P., GONZALES W.,
GLASER P., IONESCU M., LUBCCHINSKY B., MARCELINO L., MOSŽER I.,
PRESECAN E., SANTANA M., SCHNEIDER E., SCHNEIZER J., VERTES A.,
RAPOPORT G., DANCHIN A.;
"Bacillus subtilis genome project: cloning and sequencing of the
"Bacillus subtilis genome to 333 degrees.";
Mol. microbiol. 10:371-384(1993).
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STRAIN-168;
                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 95318144.
PEREGO M., GLASER P., MINUTELLO A., STRAUCH M.A., LEOPOLD K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                                EMBL; X73124; CAA51557.1; -. EMBL; Z99123; CAB15880.1; -.
                                                                                                            ACT_SITE
                                                                                                                                                                                                                        PIR; S39656;
SUBTILIST; B
                                                                                 SEQUENCE
                                                                                                                                                      Oxidoreductase
                                                                                                                                                                                                      PROSITE
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                                                                                                                                                                              PF00106;
                                    Length: 252
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(Rel. 31, Last seq
(Rel. 34, Last ann
                                                                                 152
252 AA;
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                                                                                                                                                                           61; ADH_SHORT; 1. adh_short; 1.
TGGSAGIGLE LAKRLLELGN EVIICGRSEA RLAEAKQQLP
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152
28268 >
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Last annotation updat
                                          February 14, 2000 08:02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGNELAPTGI
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                                                                                    NAD OR NADP (BY SIMILARITY).
BY SIMILARITY.
; CC2A1A1D CRC32;
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P28552:
01-DEC-1992 (Rel. 24, Created)
01-DEC-1995 (Rel. 33, Last sequence update)
15-JUL-1996 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
10JAL SPECIFICITY PROTEIN PHOSPHATASE 1 (EC 3.1.3.48)
10JAL SPECIFICITY PROTEIN PHOSPHATASE TYRI)
10JAL SPECIFICITY PROTEIN PHOSPHATASE TYRI)
10JUSP1 OR PTPN10 OR MKP1 OR CL100 OR HVH1

(EC 3.1.3.16) PHOSPHATASE

\_SEQUENCE 1.0 DUS1\_HUMAN

STANDARD;

PRT;

367

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STEER TRANSORDER TO SOCIO COCCURA REPORTED TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID DSBB_VIBAL
                                                                                DSBB_VIBAL Length: 165
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DISULFIDE BOND FORMATION PROTEIN B (DISULFIDE
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMBL outstation and the EMBL outstation on the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. By and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio alginolyticus
                                                                                                     TRANSMEM
NON_TER
SEQUENCE
                                                                                                                                                                                                               Oxidoreductase;
                                                                                                                                                                                                                       EMBL; D83728;
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                                                                                                                                               DOMAIN
TRANSMEM
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                                                                                                                                                                                          TRANSMEM
 151
                     101
                                                                                                                                        DOMAIN
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                                                                                                                                                                     RANSMEM
                                        51
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                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
                                          VAMMGVGVAA
                                                              MTILNSLNQF
VIFAGNLIAL
                      PSPFATCDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria;
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                                                                                                        165
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52
534
75
74
148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QYFLDGLKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFSLTLRHHV
                                                                                                        ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEQAPVHLSA
                                                                                                                                                                                                                Chaperone;
                                                                                                                                                                                                                                                                                                                                          LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 ALIVI
                                           IVGLMAPNNP
                                                               SKGRLSWLLL
                      VIFPSWRPLN
                                                                                   February 14, 2000 08:02
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33
51
57
74
92
                                                                                                         18745 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision;
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                                                                                                                                                                                                       Inner membrane;
CYTOPLASMIC (
                                            IFRWLGLIGW GLSSYKGLLL
                                                                LLEVVFFEAC ALYFQHVMML
                       QWAPWIFEAY
                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                 POTENTIAL
                                                                                                                                                                                   PERIPLASMIC
                                                                                                                                                                                             POTENTIAL
                                                                                                          FA018063 CRC32;
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                        GDCSKIVWQF LDLSMPQWLV
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                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                     Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OXIDOREDUCTASE)
                                                                                      Type: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKSRDKQGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAFNPLAVYP
                                             AQQHVDYQFN
                                                                    APCVMCIYER
                                                                                         Check:
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I!AA_SEQUENCE 1.0
ID DUS1_MOUSE
AC P28563;
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A KEYES S.M., EMSLIE E.A.;
T "Oxidative stress and heat shock induce a human gene encoding a RT protein tyrosine phosphatase.";
RI Nature 359:644-647(1992).
CC -: FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP CC KINASE ERKZ ON BOTH THR-183 AND TYR-185.
CC -: CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC -: SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-CC -: INDUCTION: BY OXIDATIVE STRESS AND HEAT SHOCK.
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-AL SPECIFICITY PROTEIN PHOSPHATASE 1 (EC 3.1.3.48)
(MAP KIWASE PHOSPHATASE-1) (MPR-1) (PROTEIN-TYROSINE
3CHI34) (PROTEIN-TYROSINE PHOSPHATASE DISPITED OR PTPN10 OR MKP1 OR 3CHI34 OR PTPN16.
Mus musculus (Mouse).
Eutheria; Rodentia; [1]
                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                     351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Cell cycle.
DOMAIN 175 367
ACT_SITE 258 258
SEQUENCE 367 AA; 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NSALSYLQSP
                                                                                                                                                                                                                                                                                    FMGQLLQFES
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                                                                                                                                                                                                                                                                                                                                                                                       TSVPDSAESG
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                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                   ITTSPSC
                                                                                                                                                                                                                                                                              QVLAPHCSAE AGSPAMAVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGLRALLGER AAQCLLLDCR SFFAFNAGHI AGSVNVRFST
                                                                                                                                                                                                                                                                                                                                                 PNHFEGHYQY
                                                                                                                                                                                                                                                                                                                                                                                   CSSCSTPLYD
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       Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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258 BY SIMILARITY.
39297 MW; DA323420 CRC32;
                                                                                                                                                                                                                                                                                                              AYLMRINRYK LDEAFEFVKQ
                                                                                                                                                                                                                                                                                                                                                                                                          LKGGYEAFSA SCPELCSKQS TPMGLSLPLS
                                                                                                                                                                                                                                                                                                                                               KSIPVEDNHK
                                                                                                                                                                                                                                                                                                                                                                                   QGGPVEILPF
                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                           RGTSTTTVFN FPVSIPVHST
                                                                                                                                                                                                                                                                                                                                             ADISSWENEA
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                                                                                    (EC 3.1.3.16)
PHOSPHATASE
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DUS1_MOUSE
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RX SUM H., CHARLES C.H., LAU L.F., TONKS N.K.;

RX SUM H., CHARLES C.H., LAU L.F., TONKS N.K.;

RY SUM H., CHARLES C.H., LAU L.F., TONKS N.K.;

RY SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP C. 1. INDUCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP C. 1. INDUCTION: DUAL SPECIFICITY PHOSPHATE H.(2)O = PROTEIN TYROSINE PHOSPHATE.

CC ITALLYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE H.(2)O = PROTEIN TYROSINE PHOSPHATE.

CC ITALLYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE H.(2)O = PROTEIN TYROSINE PHOSPHATE.

CC ITALLYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE.

CC ITALLYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE H.(2)O = PROTEIN TYROSINE PHOSPHATE.

CC ITALLYTIC ACTIVITY: PROTEIN THE 
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MEDITIE: 9360956.

NOGUCHI T., METZ R., CHEN L., MATTEI M.-G., CARRASCO D., BRAVO R.,

"Structure, mapping, and expression of erp, a growth factor-inducible gene encoding a nontransmembrane protein tyrosine phosphatase, and effect of ERP on cell growth.",

Mol. Cell. Biol. 13:5195-5205(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 92158357.
CHARLES C.H.; ABLER A.S., LAU L.F.;
"CDNA sequence of a growth factor-inducible immediate characterization of its encoded protein.";
Oncogene 7:187-190(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BALB/C;
                                                                                                                                                                                                                                       MVMEVGILDA GGLRALLREG
                                                                                                                                                                                                                                                                               Length: 367
                                                                                                                                                                                                                                                                                                             1/5
258
258
367
                                                                                                                                                                                                                                                                                                                    AΑ;
    QVLAPHCSAE
                                           GISRSATICL
                                                                                                                                                                                                GLEHIVPNAE
                                                                               PNHFEGHYQY
                                                                                                                                                          REARSTOVEF
                                                                                                                                                                                                                                                                    February 14, 2000 08:02 Type: P
                                                                                                                                                                                                                                                                                                                    39369
                                                                                                                                                                                                                                                                                                               C->S: LOSS
MW; 17B905B5
    AGSPAMAVLD
                                 AYLMRTNRVK LDEAFEFVKQ RRSIISPNFS
                                                                             KSIPVEDNHK
                                                                                                                   QGGPVEILSF
                                                                                                                                                          LQGGYEAFSA
                                                                                                                                                                                            LRGRLLAGAY HAVVLLDERS
                                                                                                                                                                                                                             AAQCLLLDCR SFFAFNAGHI AGSVNVRFST
RGTSTTTVFN FPVSIPVHPT
                                                                          ADISSWFNEA
                                                                                                                 LYLGSAYHAS
                                                                                                                                                       SCPELCSKQS
                                                                                                                                                                                                                                                                                                               OF ACTIVITY CRC32;
                                                                                                            RKDMLDALGI
                                                                                                                                                                                         ASLDGAKRDG
                                                                                                                                                                                                                                                                      Check:
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\_SEQUENCE 1.0 DUS1\_RAT

supplied

and

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IIAA_SEQUENCE 1.0
ID DYR1_BRARE
AC P35621;
DT 01-UUN-1994 (1)
DT 15-JUL-1999 (1)
DT 15-JUL-1999 (1)
DE DVR-1 PROTEIN
GN VG1 OR DVR-1.
OS Brachydanio rr
OC Eukaryota; Me
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 1 (EC 3.1.3.48)
(MAP KINASE PHOSPHATASE-1) (MPK-1) (PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its concent is in modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DVR-1 PROTEIN PRECURSOR.
        Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. M. SCHLEGEL W. ARKINGTALL S.;
mitted (JAN 1995) to the EMBL/Genhank/DDBJ databases.
FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES
FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES
KINASE ERK2 ON BOTH THR-183 AND TYR-185
KINASE ERK2 ON BOTH THR-183 AND TYR-185
KINASE ERK2 ON BOTH THR-183 AND TYROSINE PHOSPHATE + H(2)O -
CATALYTIC ACTIVITY: PROTEDIN TYROSINE PHOSPHATE + ONTHOPHOSPHATE.
PROTEIN TYROSINE + ORTHOPHOSPHATE.
PROTEIN TYROSINE + ORTHOPHOSPHATE.
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TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
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ota; Metazoa; Chordata;
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PS50056; TYR_PHOSPHATASE_2; 1.
PS50054; TYR_PHOSPHATASE_DUAL;
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367 1
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175, 367
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39541 MW;
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DSPc; 1.
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BY SIMILARITY:
; 9DE266E3 CRC32;
                          (Zebra danio).
Craniata; Vertebrata;
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Rattus.
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PHOSPHATASE
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                                       Actinopterygii;
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I Less requires a license.

I Send an email to licensee.

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I SENBL; U00931; AAC27347.1; -.

DR HSSP; P18075; IBMF-BETA; 1.

DR PROSITE; P500250; TGF-BETA; 1.

DR PROSITE; P500250; T
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ID E128_DROME
AC P08761;
DT 01-NOV-1988 (FDT 01-NOV-1988 (FDT 01-CT-1996 (F
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HELDE K.A., GRUNWALD D.J.;
HELDE K.A., GRUNWALD D.J.;
"The DVR-1 (Vg1) transcript of
"The DVR-1 (Vg1) transcript of
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Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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                                                    P08761;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
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SUBUNIT: HOMODIMER (PROBABLE):
SUBUNIT: HOMODIMER (PROBABLE):
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DUS1\_RAT

SEQUENCE

NIAMOC

PROSITE;

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EKNEGMQLEI

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351 301 251 restrictions

a collaboration -MBL outstation -

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MUDA M., S Submitted

OR CL100

ECDYSONE-INDUCED EIP28/29.

PROTEIN 28/29

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(Fruit fly)

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EI28_DROME Length: 255 February 14, 2000 08:02 Type: P Check:
"A novel marsupial protein expressed by the mammary gland only during the early lactation and related to the Kunitz proteinase inhibitors."; Arch. Biochem. Biophys. 330:59-64(1996).

-!- SUBCELLULAR LOCATION: SECRETED.

-!- DEVELOPMENTAL STAGE: EXPRESSED ONLY DURING EARLY LACTATION PHASE.

-!- TISSUE SPECIFICITY: EXPRESSED BY THE MAMMARY GLAND.
                                                                                                                                                                                                                                                                      ELAC_TRIVU
Q29143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X58286; CAA41223.1; -.
EMBL; X04024; CAA27655.1; -.
EMBL; X04024; CAA27658.1; -.
EMBL; X04024; CAA27658.1; -.
EMBL; X04521; CAA28205.1; -.
PIR, A24524; A24254
FLYBASE; FEBOR000565; Eip71CD.
PFAM; PF01625; PMSR; 1.
Alternative splicing.
                                                                                            SEQUENCE FROM N.A., AND S
TISSUE=MAMMARY GLAND;
PIOTTE C.P., GRIGOR M.R.;
                                                                                                                                           Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
                                                                                                                                                                                                    15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
EARLY LACTATION PROTEIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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CHERBAS L., SCHULZ R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CANTON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HERBAS L., SCHULZ R.A., KOEHLER M.M.D., SAVAKIS C., CHERBAS P.; Structure of the E1p28/29 gene, an ecdysone-inducible gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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252
255 AA;
                                                                                                                                                                                                                                                                                   STANDARD;
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82.
252
28332 MW;
                                                                                                                        AND SEQUENCE OF
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V -> L (IN MRNA).
; 61E72253 CRC32;
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IIAA_SEQUENCE 1.0
ID ERP2_YEAST
AC P39704;
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                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or.send.an.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C / AB972;

MEDILINE; 95028152.

CLARK M.W., KENG I., STORMS R.K., ZHONG W., FORTIN N., ZENG B.,

DELANEY S., OUELLETTE B.F.F., BARTON A.B., KABACK D.B., BUSSEY H.;

"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis c

the 42 kbp SPO7-CENI-CDC15 region.";

Yeast 10:535-541(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ERP2 PROTEIN PRECURSOR.
ERP2 OR YALOO7C OR FUN54.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease inhibitor; S
SIGNAL
1 20
CHAIN
2 102
DISULFID 23
DISULFID 52 76
DISULFID 52 76
DISULFID 68 89
ACT_SITE 53 54
CARBOHYD 34
C
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DISULFID
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SEQUENCE
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
D7983676 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Lactation.
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                                                                     There are no restrictions on ng as its content is in no
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                                                                                                                        a collaboration war. outstation -
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SO SO
                                                                                ERP2_YEAST
                                                            ES1_BRARE
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ES1_BRARE
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PIR; $40896; $40896;

SGD; L0004679; ERP2.

PFAM; PF01105; EMP24_GP25L;
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                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterydi; Teleostei; Buteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                                             EMBL; U10403; AAC60261.1; TES1. ZFIN; ZDB-GENE-980526-188; ES1. Mitochondrion; Transit peptide. TRANSIT 1 7 MI
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                                         MLASRALLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein transport;
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1 25
26 215
26 182
183 203
204 215
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S40896.
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                                                                                    PΑ;
                                           QAAAMLVRQP
MMQMNDLSKL DANSFDAVIF PGGHGIVKNM STFSKDGKDO
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                                                              February 14,
                                                                                    270
30685 MW;
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                                           ACLMHHGGDW
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LUMENAL (POTENTIAL).
POTENTIAL.
                     QIFAPNQQQM
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                                                                                                MITOCHONDRION (POTENTIAL).
ES1 PROTEIN.
                                                                                      181 PROTEIN.
4B69565D,C
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                                            GNWGNTNIAV VFSGCGWWDG
                        HVMDHMKMQP
                                                                                        CRC32;
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                                                                 Type:
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                         SSSDNRNIM
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                                                                    Check:
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                                                                                                                                                                                                                              a collaboration -
                                                                                                                                                                                                                           outstation
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Bacteria; [1]

beta

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ETFA_MYCLE Length:
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15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel.
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EMBL; Z99263; CAB16419.1; 1.
PROSITE; PS00696; ETF_ALPHA; 1.
PFAM; PF00766; ETF_AlPha; 1.
F1avoprotein; FAD. (ADP PART) (POTENTIAL)
F1action transport; F1avoprotein; F1avoprotein
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15-DEC-1998 (Rel. 37, Last seq
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                                gonorrhoeae.
proteobacteria;
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annotation
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                                            subdivision; Neisseriaceae;
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EXBD_NEIGO Length: 144 February 14, 2000 08:02
                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-SEROGROUP C;

MEDLINE; 97158676.

MEDLINE; 97158676.

STOJILJKOVIC I., SRINIVASAN N.;

"Nelsseria meningitidis tonB, exbB, and exbD genes: Ton-dependent utilization of protein-bound iron in Neisseriae.";

J. Bacteriol. 179:805-812(1997).

J. Bacteriol. 179:805-812(1997).

TEUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).

TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).

COMPLEX WITH TONB (BY SIMILARITY).

TOMPLEX WITH TONB (BY SIMILARITY).
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                                                                                                                           (PROBABLE).
-!- SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                       Neisseria
Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U79563; AAC45288.1; ..

Transport; Protein transport; Transmembrane; Inner membrane.
DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
TRANSMEM 19 39 POTENTIAL.
DOMAIN 40 144 PERIPLASMIC (POTENTIAL).
TRANSMEM 40 144 PERIPLASMIC (POTENTIAL).
TRANSMEM 40 144 PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                          EXBD_NEIME STANDARD; PRT; 195376; PS5376; Created) 15-DEC-1998 (Rel. 37, Last sequence up 15-DEC-1998 (Rel. 37, Last annotation BIOPCLYMER TRANSPORT EXBD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                       EXBD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
STRAIN=FA19;
MEDLINE; 9728
MEDLINE; 9728
DISWAS G.D.,
"Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tonB, exbB
Mol. Microb
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oning and functional characterization of Neisseria gonorrhoeae
1B, exbB and exbD genes.";
1. Microbiol. 24:169-179(1997).
1. Microbiol. 24:169-179(1997).
1. FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT
TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).
1. SUBGULIT: THE ACCESSORY PROTEINS EXBB AND EXBD SEEM TO FORM A
1. COMPLEX WITH TONB (BY SIMILARITY).
1. SUBGEELULAR LOCATION: TYPE II MEMBRANE PROTEIN. INNER MEMBRANE
              U77738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FROMENEL).
SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                    meningitidis.
Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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                                                                                                                              SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR).
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EMBL; M84991; AAA23739.1;

There are no restrictions on ng as its content is in no

collaboration -

for

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EXBD_NEIME Length: 144 February 14, 2000
                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-KI2;

MEDIJINE, 97061202.

MEDIJINE, 97061202.

OSHIMA T., AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A.,

OSHIMA T., AIBA H., JTOH T., KAJIHARA M., KANAI K., KASHIMOTO K.,

IKEMOTO K., INADA T., ITOH T., KAJIHARA M., KANAI K., KASHIMOTO K.,

KIMURA S., KITAGAWA M., MAKINO K., WASUDA S., MIKI T., MIZOBUCHI K.,

KIMURA S., KITAGAWA K., NAKANURA Y., NASHIMOTO H., NISHIO Y.,

MORI H., MOTOMURA K., NAKANURA Y., NASHIMOTO H., NISHIO Y.,

SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y.,

YAND M., HORIUCHI T.,
SAMPEI G., SEXI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M., HORITCHI T., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., "A 7.18-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.", DNA RES. 3:137-155(1996).

-I- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] H. MADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.

-I- PATHMAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHMAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     "The com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
MEDLINE; 97426617.
BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92210530.

RAWLINGS M., CRONAN J.E. JR.;

"The gene encoding Escherichia coli acyl carrier
a cluster of fatty acid biosynthetic genes.";

J. Biol. Chem. 267:5751-5754(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P25716; p78221;
01-MAY 1992 (Rel. 22, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-CARRIER PROTEIN REDUCTASE).
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STRAIN-K12;
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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15514 MW;
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
6347F02B CRC32;
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THE TRANSPORT OF THE PROPERTY 
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EMBL; D90745; BA
PIR; B42147; B42
HSSP; P19992; 2H
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
3-OXOACYL-(ACYL-CARRIER PROTEIN| REDUCTASE (EC
ACYL CARRIER PROTEIN REDUCTASE).
EABG OR HI0155
                           EMBL; U32701;
HSSP; P19992;
TIGR; HI0155;
                                                                                                                                                                                                                                                                                                                                                                                                                 FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BUIT C.J., TOMB J.-F., DOUGHERRY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WELDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., FINE L.D., KELLEY J.M., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1.0
FABG_HAEIN
                                                                                                                        use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no ways by non-profit institutions as long as its content.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VENTER J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole-genome random sequencing and assembly of Haemophilus
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   PS00061; ADH_SHORT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; B42147
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BAA35901.1;
                                                                             AAC21824.1;
                                                       2HSD.
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BY SIMILARITY.
A -> G (IN REF. 1).
; 07319E62 CRC32;
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SOTER
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                                                                                                                                                        FABG_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PAO1;

KUTCHNA A.J., HOANG T.T., SCHWEIZER H.P.;

KUTCHNA PAO1;

SUBMILTEG (FEB-1997) to the EMBL/GenBank/DDBJ databases.

PAON (ARTICLE FEB 18 TO THE FATTY ACID BIOSY MADP(+) = 3-0X0ACYL-[ACYL-CARRIER PROTEIN] + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 1.0
FABG_PSEAE
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PFAM; PF00678; adh_short_C2; 1.
Fatty acid biosynthesis; Oxidoreductase; NADP.
NP_BIND 8 2 NADP (BY SIMILARITY)
RCT_SITE 149 149 BY SIMILARITY.
SEQUENCE 242 AA; 25507 MW; CBFCAFD9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb.sorsend an email to license@isb.sib.ch).
                                                                                                                                                                                                       EMBL; U91631; AAB94395.1; -.

PROSITIE; PS00061; ADH_SHORT; 1.

PFAM; PF00106; adh_short_C2; 1.

FFATY acid biosynthesis; Oxidoreductase; Oxid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (ECARYL CARRIER PROTEIN REDUCTASE).
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                                                                                                     MSLQGKVALV TGASRGIGQA
                                                                                                                                                           Length: 247
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                                                                                                                                                    February 14,
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                                                                                                        IALELGRUGA VVIGTATSAS GAEKIAETLK
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SKAVLRGMTK
                                                     ATLEHIQQHL
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ARWGRIINIG
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                                                                                                                                                           Type: P
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   SVVGAMGNAG
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for commercial
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!!AA\_SEQUENCE 1.0

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                                                                                                                                                                                                  P28861; p11007;
01-JUL-1989 (Rel. 11, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Cast annotation update)
(FLRR) (FLDR) (METHYL VIOLOGEN RESISTANCE PROTEIN
FOR OR MYRA.
Escherichia coli.
                             SEQUENCE FROM N.A.,
STRAIN=K12 / C600;
STRAIN=K12 / C600;
MEDLINE; 93194782.
BIANCHI V., REICHARI
                                                                                                                                                                                                                                                                                                                                                                                                                 _SEQUENCE 1.0
FENR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U39441; AAC43589.1; -.
HSSP; P1992; 2HSD.
PROSITE; P500061; ADH_SHORT; 1.
PFAM; PF00106; adh_Short; 1.
PFAM; PF0078; adh_Short_C2; 1.
PFAM; PF00678; adh_Short_C2; 1.
Fatty acid biosynthesis; Oxioneductase; NADP.
NP_BIND 10 34 NADP (BY SIMILARITY).
ACT_SITE 151 151 BY SIMILARITY.
SEQUENCE 244 AA; 25519 MW; AE981EDC CRC32;
                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a content of the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.orm.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201
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"Isolation of Vibrio harvey1 acyl carrier protein and the fabG, ac and fabF genes involved in fatty acid biosynthesis.";
J. Bacteriol. 178:571-573(1996).
-i- CATALYTIC ACTIVITY: (3R)-3-4TDROXYACYL-[ACYL-CARRIER PROTEIN]
-NADP(+) = 3-OXOACYL-ACYL-CARRIER PROTEIN] + NADPH.
-i- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-B392;
MEDLINE; 96134997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio harveyi.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
3-OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE (ECACYL CARRIER PROTEIN REDUCTASE).
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P55336;
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  H:,
REICHARD P., ELIASSON R.,
., HAGGARD-LJUNGQUIST E.;
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                    AND
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                                                                                                    SEQUENCE
                                                                                                                                                                                gamma subdivision;
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                       E.
                                                                                                                                                                              Enterobacteriaceae;
                                                                                                                                                                                                                                                 (FLAVODOXIN REDUCTASE) SIN A) (DA1).
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EMBL; 104757; AAA23805.1; -EMBL; 119201; AAB03056.1; -EMBL; AE000467; AAC79506.1; -EMBL; AE000467; AAC79506.1; -EMBL; A11767; -: NOT\_ANNOTATED\_CDS.
EMBL; M19644; AAA24189.1; ALT\_SEQ.
PIR; A26225; A266225.
PIR; A462248; B45248.
PIR; A47077; A47077.
PIR; S40867; S40867.

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                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and characterization of Escherichia coli K-12.";
Of Bacteriol. 170:2136-2142(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAID-K12 / MCG100;
MEDLINE; 93015762
TRUNIGER V. BOOS W. SWEET G.;
"Molecular analysis of the glpFKX
Shigella flexner: ",
J. Bacteriol. 174:6981-6991(1992).
                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                     JENKINS C.M., WATERMAN M.R.; Plavodoxin reductase from Escherichia coli Frlavodoxin and NADPH-flavodoxin reductase from Escherichia coli support bovine cytochrome P450c17 hydroxylase activities."; J. Biol. Chem. 269:27401-27408(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-13.
MEDLINE; 95050480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 88
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PLUNKETT G. III, BURLAND V.D., DANIELS D.L., B.

"Analysis of the Escherichia coli genome. III.

region from 87.2 to 89.2 minutes.";

Nucleic Acids Res. 21:3391-3398(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Escherichia coli ferredoxin NADP+ anaerobic ribonucleotide reduction, overexpression of the protein.";
J. Bacteriol. 175:1590-1595(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY SEQUENCE OF 1-134 FROM
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STRAIN=K12 / N
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AYSYVNSPDN

PDLEFYLVTV PDGKLSPRLA ALKPGDEVQV VSETAGFFVL

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FENR_ECOLI Length: 247 February 14, 2000
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ECOGENE; EG11518; FPR.
PFAM; PF00175; oxidored_fad; 1.
Oxidoreductase; Flavoprotein; NADP; FAD; 3D-structure.
INIT_MET 0
NP_BIND 49 75
NP_BIND 109 75
SPOTENCE 109
                                                                                                                                                                                                                                                                                                  "Molecular analysis of the glpFKX regions of Escherichia coli and Shigella flexner1.";

J. Bacteriol. 174:6981-6991 (1992).

J. Bacteriol. 176:5981-6991 (1992).

-i. FUNCTION: TOGETHER WITH FLAVODOXIN IS INVOLVED IN THE REDUCTIVE ACTIVATION OF COBALAMIN. INDEPENDENT METHIONINE SYNTHASE, PYROVATE FORMATE LYASE AND ANAEROBIC RIBONUCLEOTIDE REDUCTASE. ALSO PROTECTS AGAINST SUPEROXIDE RADICALS DE TO METHYL VIOLOGEN IN THE PRESENCE OF OXYGEN (BY SIMILARITY).

-i. CATALYTIC ACTIVITY: REDUCED FERREDOXIN + NADP(+) - OXIDIZED FERREDOXIN + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FERREDOXIN--NADP REDUCTASE (EC 1.18.1.2) (FNR) (FLXR) (METHYL VIOLOGEN RESISTANCE PROTEIN A) (FPR OR MVRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P28901;
01-DEC-1992 (Rel. 24, Created)
01-JUL-1993 (Rel. 26, Last seq
15-DEC-1998 (Rel. 37, Last ann
FERREDOXIN--NADP REDUCTASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1.0
FENR_SHIFL
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Oxidoreductase; Flavoprotein; NADP; FAD. NP_BIND 50 76 FAD (BY SIM NP_BIND 110 126 NADP (RIBOS NON_TER 135 135 SEQUENCE 135 AA; 14878 MW; F6A7AD5D
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMEL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
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                                                                          PIR; S23906; S23906.
HSSP; P28861; 1FDR.
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247 AA;
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125 N.
27620 MW;
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   F6A7AD5D CRC32;
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(RIBOSE PART)
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L outstation -
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FENR\_SHIFL Length: 135

February 14,

2000

08:02

Type:

Salmonella typhimurium. Bacteria; Proteobacteria;

gamma

subdivision; Enterobacteriaceae;

MADWVTGKVT KVQNWTDALF SLTVHAPVLP FTAGQFTKLG LEIDGERVQF

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FIBR_AGKCO Length: 203
                                                                                                  _SEQUENCE 1.0
FIMH_SALTY
P37925;
01-OCT-1994 (
01-OCT-1994 (
15-DEC-1998)
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MEDLINE; 9278288.

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MARKLAND F.S. JR., MASIARZ F.R.;

MARKLAND F.S. JR., MASIARZ F.R.;

MARKLAND F.S. JR., MASIARZ F.R.;

"Amino acid sequence of fibrolase, a direct-acting fibrinolytic enzyme from Agkistrodon contortrix contortrix venom.";

Protein Sci. 1:590-600(1922).

PROTEIN IS A ZINC PROTEASE FROM SNAKE VENOM THAT ACTS IN HEMORRHAGE IT CLEAVAGE OF 14-ALA-|-LEU-15 IN INSULIN B CHARLYTIC ACTIVITY: CLEAVAGE OF 14-ALA-|-LEU-15 IN INSULIN B CHARLYTY: BELONGS TO PEPPIDASE FRAMILY M12B CINC

PROTEIN CORPORTS BILDS ONE ZINC ION.

PEPPIDASE FRAMILY M12B CINC

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01-DEC-1992 (Rel. 24, Created)
01-DEC-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
FIBROLASE (EC 3.4.24.72) (FIBRINOLYTIC PROTEINASE).
Agkistrodon contortrix contortrix (Southern copperhead).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotal
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(Rel. 30, L:
(Rel. 37, L:
(N PRECURSOR.
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30, Last sequences, Last annotations.
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144
153
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189
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                                                                                                       sequence update) annotation update;
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ZINC (CATALYTIC)
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SOME % OF THE CHAINS).
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MEDLINE; 91258343.

ALBERTINI A.M., CARAMORI T., CRABB W.D., SCOFFONE F., GALIZZI A.;

"The flaa locus of Bacillus subtilis is part of a large operon coding for flagellar structures, motility functions, and an Arpase-like polypeptide.",

Delypeptide.",

J. Bacteriol. 173:3573-3579(1991).

-!- FUNCTION: NEEDED FOR FLAGELLAR REGROWTH AND ALSO TO FIIJ.

-!- SIMILARITY: TO FLIH IN OTHER BACTERIA AND ALSO TO FIIJ.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SERVENCON D.L., CLEGG S.;

SUBMITTER (JUN-1993) to the EMBL/GenBank/DDBJ databases.

SUBMITTION: INVOLVED IN REGULATION OF LENGTH AND MEDIATION OF ADHESION OF TYPE 1 FIMBRIAE (BUT NOT NECESSARY FOR THE PRODUCTION OF FIMBRIAE). SEEMS TO BE MANNOSE BINDING ADHESIN.

OF FIMBRIAE). SEEMS TO THE FIMH / LEFD FAMILY.

SIMILARITY: BELONGS TO THE FIMH / LEFD FAMILY.

TO SIMILARITY: BELONGS TO THE FIMH / LEFD FAMILY.

THE SIMILARITY: BELONGS TO THE FIMH / LEFD FAMILY.

THE STATISHING AND THE SEMEL OUTSEAST OUTSEAST
                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bactillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
PROBABLE FLAGELLAR ASSEMBLY PROTEIN FLIH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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23
335 AA;
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335 F:
; 36056 MW;
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FIMH PROTEIN.
; 2C61967B CRC32;
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EMBL; X56049; CAA39522.1; -. EMBL; Z99112; CAB13496.1; -.

!!AA\_SEQUENCE 1.0

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II AA_SEQUENCE 1.0

ID FOS_AVINK
AC 223050;
DT 01-NOV-1991 (F
DT 01-NOV-1991 (F
DT 01-OCT-1994 (F
DT 0
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SEQUENCE FROM N.A.

MEDLINE; 88063920.

NISHIZAWA M., GOTO N., KAWAI S.;

"An avian transforming retrovirus isolated from a nephroblastoma that carries the fos gene as the oncogene.";

J. Virol. 61:3733-3740(1987).

-1- SIMILARITY: TO OTHER BZIP PROTEINS.

-1- SIMILARITY: TO OTHER BZIP PROTEINS.

-1- SIMILARITY: TO OTHER BZIP PROTEINS.
                                                                                                                 201
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                                                                                                                                                                                                                                   101
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PIR; B34071; TVFVF4.

HSSP; P01100; IFOS.

HSSP; P01100; IFOS.

HSSP; P01100; IFOS.

FRANGEAC; T01453;

PROSITE; P500036; BZIP_BASIC; 1.

PFAM; PF00170; bZIP; 1.

FTAMSFORMING Protein; Nuclear protein; Phosphorylation; DNA-binding.

DNA_BIND 93 114

BASIC MOTIF.

DOMAIN 119 147

LEUCINE-ZIPPER.

SEQUENCE 322 AA; 34333 MW; 7889C9B1 CRC32;
                                                       251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entitied and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation updat
P55-V-FOS TRANSFORMING PROTEIN.
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Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
[1]
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PIR; C42365; C42365.
SUBTILIST; BG10242; FLIH.
Flagella.
SEQUENCE 208 AA; 23788
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RKGSSSNEPS
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                                                                                                                 AVPPKEPSGS
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SDSLSSPTLL
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FOS_CHICK
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P11939;
01-OCT-1989
01-OCT-1989
01-OCT-1986
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TRANSFAC; T001
PROSITE; PS000
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SEQUENCE FROM N.A.

REDLINE: 88062957.

FUJIMARA K.T., ASHIDA K., NISHINA H., IBA H., MIYAJIMA N.,

FUJIMARA K.T., ASHIDA K.,

NISHIZAWA M., KAWAI S.;

"The chicken c-fos gene: cloning and nucleotide sequence analysis.";

J. Virol. 61:4012-4018(1987).

-!- FUNCTION: C-FOS IS A NUCLEAR PHOSPHOPROTEIN WHICH FORM A TIGHT BUTTON COVALENTLY LINKED COMPLEX WITH THE C-JUN/AP-1 TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOELDERS H., JENUWEIN T., ADAMKIEWICZ J., MUELLER R.;
"Isolation and structural analysis of a biologically active chicken c-fos cDNA: identification of evolutionarily conserved domains in fos protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence up
01-OCT-1986 (Rel. 34, Last annotation
p55-C-FOS PROTO-ONCOGENE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M37000; AAA48670.1; -.
EMBL; M18043; AAA76823.1; -.
PIR; A28368; TVCHFS.
HSSP; P01100; 1FOS.
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Eukaryota: Metazoa, Chordata: Craniata: Vertebrata: Archosauria; Aves:
Neognathae: Galliformes; Phasianidae: Phasianinae: Gallus.
301
                                 251
                                                                 201
                                                                                                 151
                                                                                                                               101
                                                                                                                                                                                                                                                        Proto-oncogene; Nuclear protein; Phosphorylation;
DNA_BIND 138 159 BASIC MOTIF.
DONAIN 164 192 LEUCINE-ZIPPER.
CONFLICT 90 90 N -> D (IN REF. 2).
SEQUENCE 367 AA; 39004 MW; AJFCDACB CRC32;
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00036; BZIP_BASIC; 1.
PFAM; PF00170; bZIP; 1.
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EDLINE: 88262231.
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INDUCTION: C-FOS EXPRESSION INCREASES RAPIDLY UPON GROWTH FACTOR STIMULATION OR WOUNDING OF CULTURED CELLS.
SIMILARITY: TO OTHER BZIP PROTEINS.
                                                                                                                             APPAAYSRPA VLKAPGGRGQ
                                                                                                                                                                                             MMYQGFAGEY EAPSSRCSSA
                                                                 PACKMPEELR
                                                                                                                                                               TDLAVSSANF
                                                                                                                                                                                                                         Length: 367
 AGSGGELEPL CTPVVTCTPC
                                 EPSGSGLELK
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                                                                 FSEELAAATA
                                                                                                                                                               VPTVTAISTS
                                 AEPFDELLFS
                                                                                               TOTLQAETDQ
                                                                                                                                                                                                                            February 14, 2000 08:02 Type: P
                                                                                                                             SIGRRGKVEQ
 PSTYTSTFVF TYPEADAFPS CAAAHRKGSS
                                 AGPREASRSV
                                                                 LDLGAPSPAA
                                                                                               LEEEKSALQA
                                                                                                                                                               PDLQWLVQPT
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on update)
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                                                                                                                               LSPEEEEKRR
                                 PDMDLPGASS
                                                                 AEEAFALPLM
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                                   FYASDWEPLG
                                                                                                                                                                                              GSPVNSQDFC
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                                                                                                                                 IRRERNKMAA
                                                                                                                                                               RGHPYGVPAP
                                                                 TEAPPAVPPK
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                                                                                                                                                                                                                            Check: 7007
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!!AA\_SEQUENCE 1.0

351

SPTLLAL

!!AA\_SEQUENCE 1.0

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STTREET OF STREET STREE
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MEDLINE; 83221560.
WILLER R., CURRAN T., VAN BEVEREN
VAN STRAATEN F., WILLER R., CURRAN T., VAN BEVEREN
"Complete nucleotide sequence of a human c-oco gene
acid sequence of the human c-fos protein.";
proc. Natl. Acad. Sci. U.S.A. 80:3183-3187(1983).
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PO1100;
PO1100;
PO1100;
PO1100;
PO1-1986 (Rel. 01, Created)
PO1-1986 (Rel. 01, Last sequence update)
PO1-NOV-1997 (Rel. 35, Last annotation update)
PO5-C-FOS PROTO-ONCOGENE PROTEIN (GOS7 PROTEIN)
351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; V01512; CAA24756.1; -.
EMBL; K00550; AAA52471.1; -.
PIR; A01342; TVHUF1
PDB; 1FOS; 10-JUL-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- INDUCTION: C-FOS EXPRESSION INCREASES RAPIDLY UPON GROWTH FACTOR STIMULATION OR WOUNDING OF CULTURED CELLS.
-!- SIMILARIYY: TO OTHER BLIP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLOVER J.N., HARRISON S.C.;
"Crystal structure of the heterodimeric bZIP
"-FOS-c-Jun bound to DNA.";
Nature 373:257-261(1995).
"I- FUNCTION: C-FOS IS A NUCLEAR PHOSPHOPROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iomo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Ve.
Sutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EDLINE;
                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF 139-198 IN COMPLEX WITH JUN
                                                                                                                                                                                                                                                                                                                                                                       μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coto-oncogene; Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: C-FOS IS A NUCLEAR PHOSPHOPROTEIN WHICH NON-COVALENTLY LINKED COMPLEX WITH THE C-JUN/AP-1
FPSCAAAHRK
                                                                                                                                                                                                                                                                                                                                                                              MMFSGFNADY
                                                     ADWEPLHSGS
                                                                                                                                                                                                                                                                   PSAGAYSRAG
                                                                                                                                                                                                                                                                                                                        TDLAVSSANF IPTVTAISTS
                                                                                                       PSVEPVKSIS
                                                                                                                                                                                                                 AAKCRNRRRE
                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00036; BZIP_BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165
380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
GSSSNEPSSD SLSSPTLLAL
                                                                                                                                                                                                                                                                                                                                                                              EASSSRCSSA
                                                                                                                                                                                                                 LIDILQAEID
                                                                                                                                                                                                                                                                   VVKTMTGGRA
                                                     LGMGPMATEL
                                                                                                          SMELKTEPFD
                                                                                                                                                            GFPEEMSVAS
                                                                                                                                                                                                                                                                                                                                                                                                                             February 14, 2000 08:02 Type: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160
193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40695 MW;
                                                  EPLCTPVVTC
                                                                                                                                                            LDLTGGLPEV
                                                                                                                                                                                                                 QLEDEKSALQ
                                                                                                                                                                                                                                                                   QSIGRRGKVE
                                                                                                                                                                                                                                                                                                                        PDLQWLVQPA LVSSVAPSQT
                                                                                                                                                                                                                                                                                                                                                                          SPAGDSLSYY HSPADSFSSM GSPVNAQDFC
                                                                                                          DFLFPASSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASIC MOTIF.
LEUCINE-ZIPPER.
; CDDAEF5C CRC32;
                                                                                                                                                                                                                 TETANLLKEK
                                                                                                                                                                                                                                                                   QLSPEEEEKR
                                                     TPSCTAYTSS
                                                                                                          SGSETARSVP
                                                                                                                                                               ATPESEEAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene:
                                                                                                                                                                                                                                                                      RIRRERNKMA
                                                                                                          DMDLSGSFYA
                                                                                                                                                                                                                    EKLEFILAAH
                                                                                                                                                                                                                                                                                                                        RAPHPFGVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                   Check:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor
                                                                                                                                                                                                                                                                                                                                                                                                                                      4677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
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BUT

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I DAA AC DIT DE DE DE OC OC
                                                                                                                                                                                                                                                                                                                                                FTRC_MAIZE Length: 152
METAL
DISULFID
METAL
METAL
METAL
SEQUENCE
                                                                                                                                                                                                        151
                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSIT
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOCHIM. BIOPHYS. Acta 1183:207-209(1993).

I: FUNCTION: FTR IS A [4FE-46] PROTEIN PLAYING A CENTRAL ROLE IN THE FERREDOXIN/THIOREDOXIN REGULATIORY CHAIN. IT CONVERTS AN ELECTRON SIGNAL (PHOTOREDUCED FERREDOXIN) TO A THIOL SIGNAL (REDUCED THIOREDOXIN) IN THE REGULATION OF ENZYMES BY REDUCTION OF SPECIFIC SECURAL PHOTOSYNTHETIC ENZYMES.

SEVERAL PHOTOSYNTHETIC BNZYMES.

I: SUBUNIT: HETERODIMER OF SUBUNIT A (VARIABLE SUBUNIT) AND SUBUNIT B (CATALYTIC SUBUNIT).

B (CATALYTIC SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAIZEDB; 61547; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
(EC 1.18.-.-) (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE; 94002243.

MARC-MARRIN S., SPIELMANN A., STUTZ E., SCHUERMANN P.;

"Cloning and sequencing of a corn (Zea mays) nuclear gene coding for "Cloning and sequencing of a corn (Zea mays) nuclear gene coding for the chloroplast specific catalytic subunit of ferredoxin-thioredoxin
                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              žea mays (Maize).
Žukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTRC_MAIZE P41347;
                                                                                                                                                                                                                                   AEVAQGFWNC
                                                                                                                                                                                                                                                         RKFSEQYARR SNTFFCADKT VTAVVIKGLA DHRDTLGAPL CPCRHYDDKA
                                                                                                                                                                                                                                                                                      MISTVITTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X73549; -; NOT_ANNOTATED_CDS.
DB; 61547; -.
                                                                                                                                                                                                                                                                                                                                                           91
93
110
112
121
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                                                                                                                                                                                                                                 PCVPMRERKE CHCMLFLTPD
                                                                                                                                                                                                                                                                                      CGGLPVRPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                           121
16740
                                                                                                                                                                                                                                                                                                                                                                        91
123
110
112
                                                                                                                                                                                                                                                                                                                 February 14, 2000
                                                                                                                                                                                                                                                                                                                                            WW.
                                                                                                                                                                                                                                                                                      TATRGRPRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                    4Fe-4S; Chloroplast; Transit peptide CHLOROPLAST (BY SIMILARITY). FERREDOXIN-THIOREDOXIN REDUCTASE,
                                                                                                                                                                                                                                                                                                                                                        IRON-SULFUR (4FE-4S) (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                            25FEEF37
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                                                                                                                                                                                                                                NDFAGKDQVI
                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                            CRC32;
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51

MQKLQISVYI YLFTLIVAGP SRLEAIKIQI LSKLRLETAP

VDLNENSEQK NISKDAIRQL

ENVEKEGLCN LPKAPPLLEL

ACLWRENTTS IDQFDVQRDA

151 201

LVKAQLWIYL RPVKTPATVF VQILRLIKPM

KDGTRYTGIR

SEKEDMNPGT

SNLGIEIKAL

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ORGERY REPRESENTATION OF SOME 
       GDF8_BOVIN
                                                                                                                                                                                                                                                          Or send au .....

EMBL: AF019761; AAR81508.1; -.

EMBL: AF019620; AAR86687.1; -.

HSSP; P18075; IBMP.

PROSITE: P500250; TGF_BETA; 1.

PFAM; PF00019; TGF_beta; 1.

PFAM; PF00019; TGF_beta; 1.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.
                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
STRAIN=HOLSTEIN; TIS
MEDLINE; 98024153.
MCPHERRON A.C., LEE
"Double muscling in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISG-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FRIESIAN; T
MEDLINE; 97458167.
KAMBADUR R., SHARM
"Mutations in myos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovinae;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT MH TYR-313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERFON A.C., LEE S.-J.;
le muscling in cattle due to m
Natl. Acad. Sci. U.S.A. 94:12
UNCTION: ACTS SPECIFICALLY AS
       Length: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos
                                                   375
                                                                                                                   267
281
309
313
339
47
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A., AND VARIANTS MH LEU-94
TISSUE-SKELETAL MUSCLE;
     February 14, 2000
                                                   MW;
                                                                     E -> K (IN C -> K (IN
                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
CONTROL (BY SIMILARITY).
                                                                                                                                    POTENTIAL.
                                                F97E649A
                                                                                                                                                                                                                                                OWTH/DIFFERENTIATION SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to mutations in the myostatin gene."; 4:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A NEGATIVE
08:02 Type: P
                                              N MH; PIEDMONTESE | N MH; PIEDMONTESE | N REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGULATOR
     Check:
                                                                                         BREED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blue
     9403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
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PELEVKVTDT

PKRSRRDFGL DCDEHSTESR CCRYPLTVDF EAFGWDWIIA

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GDF8_HUMAN Length: 375
ID GDF8_MOUSE
                                                                                                                                                                                                                                                                                                                                                                           Growth factor;
SIGNAL 1
PROPEP 267
CHAIN 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EM purposen Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorseid an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDF8 OR MSTN.
HOMO sapiens (Human).
Homo sapiens (Human).
Traniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8)
                                                                                                                                                                                                                                                                                                                       DISULFID DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98024153.

MCPHERRON A.C., LEE S.-J.;

"Double muscling in cattle due to mutations in the myostatin gene.";

"Double muscling in cattle due to mutations in the myostatin gene.";

Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

-I- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS002
PFAM; PF00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF019627; AAB86694.1; -. MIM; 601788; -.
                                        351
                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE-SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYFNGEGQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                     MQKLQLCVYI YLFMLIVAGP VDLNENSEQK ENVEKEGLCN ACTWRQNTKS
                                      LYFNGKEQII YGKIPAMVVD
                                                                    PKRYKANYCS
                                                                                                                                                                                                                                                                                                                                                                                                            PS00250; TGF_BETA; 1.
00019; TGF-beta; 1.
00019; TGF-beta; 1.
actor; Cytokine; Glycoprotein; Signal.
1 ? POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGKIPAMVVD RCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GECEFVFLQK YPHTHLVHQA NPRGSAGPCC TPTKMSPINM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUSCLE;
 STANDARD;
                                                                                                                                                                                                            LSKLRLETAP
                                                                                                                           VLQNWLKQPE
                                                                                                                                                       RPVETPTTVF
                                                                                                                                                                                 YHATTETIIT
                                                                    GECEFVFLQK
                                                                                                                                                                                                                                                                                                                       375
375
372
374
339
                                                                                                                                                                                                                                                                February 14, 2000 08:02 Type: P Check:
                                                                                                                                                                                                                                                                                             42750 MW;
                                                                                                                             SNLGIEIKAL
                                                                                                                                                       VQILRLIKPM
                                                                                                                                                                                 MPTESDFLMQ VDGKPKCCFF
                                                                                                                                                                                                           NISKDVIRQL LPKAPPLREL
                                                                                                 DCDEHSTESR
                                                                     YPHTHLVHQA
                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
GROWIN/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                       INTERCHAIN (BY SIMILARITY)
   PRT;
                                                                                                                                                                                                                                                                                               D0EC1323 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375
    376
                                                                     NPRGSAGPCC TPTKMSPINM
                                                                                                                             DENGHDLAVT
                                                                                                                                                       KDGTRYTGIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                 CCRYPLIVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions on ng as its content is in no
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                                                                                                                                                        SLKLDMNPGI
                                                                                                                                                                                    KESSKIQYNK
                                                                                                                             FPGPGEDGLN
                                                                                                                                                                                                              IDQYDVQRDD
                                                                                                 EAFGWDWIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MYOSTATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                     1814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outstation
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GDF8_MOUSE
ID GDF8_PAPHA
                                                                                                                                                                                                                                                                                                                                                                                      Growth factor; Cytokine; G. SIGNAL 1
PROPER 1
PROPER 1
PROPER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O08689;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Regulation of skeletal muscle mass in n superfamily member.";
Nature 387:83-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

-I- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND AD

-I- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND AD

-I- DEVELOPMENTAL MYSCLE, WEAK EXPRESSION IN ADIPOSE TISSUE

-I- DEVELOPMENTAL STAGE: FIRST DEFECTED AT DAY 9.5 POST-COITUM IN

ONE-THIRD OF DEVELOPING SOMITIES. AT LATER STAGES OF DEVELOPMENT,

DETECTED IN A WIDE BANGE OF DEVELOPING MUSCLES. EXPRESSION
                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
DISULFID
CARBOARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U84005; AAC53167.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CD-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                  (SSP) p18075; .....

(GD) MGI:95691; MSTN.

(GD) MGI:95691; MSTN.

PROSITE; PS00250; TGF_BETA; 1.

PFAM; PF00019; TGF-beta; 1.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTINUES IN ADULTHOOD.
                                            351
                                                                    301
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUSCLE GROWTH
                                          MLYFNGKEQI
                                                                                                                                                                                                                                        MMQKLQMYVY IYLFMLIAAG
                                                                      APKRYKANYC
                                                                                                  NPFLEVKVTD
                                                                                                                                                                                                              YSRIEAIKIQ
                                                                                                                                                                                                                                                                Length: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lus (Mouse).
, Metazoa; Chordata; Craniata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                               376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                               AA;
   STANDARD;
                                                                                                                                                         LRPVKTPTTV
                                                                                                                                                                                   DYHATTETII
                                                                                                                                                                                                              ILSKLRLETA PNISKDAIRQ LLPRAPPLRE LIDQYDVQRD
                                          IYGKIPAMVV
                                                                      SGECEFVFLQ
                                                                                                   TPKRSRRDFG
                                                                                                                             TYLQNWLKQP
                                                                                                                                                                                                                                                                                            72
42921 MW;
                                                                                                                                                                                                                                                                    February 14, 2000 08:02 Type: P Check:
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EXPRESSED SPECIFICALLY IN DEVELOR
                                            DRCGCS
                                                                      KYPHTHLVHQ
                                                                                                   LDCDEHSTES
                                                                                                                             ESNLGIEIKA
                                                                                                                                                         FVQILRLIKP
                                                                                                                                                                                   TMPTESDFLM
                                                                                                                                                                                                                                         PVDLNEGSER EENVEKEGLC NACAWRQNTR
                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
GROWTH/DIFFERENTIATION F
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                            POTENTIAL.; F11ED196 CRC32;
                                                                                                                                                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY)
    PRT;
    375
                                                                                                                                                           MKDGTRYTGI
                                                                         ANPRGSAGPC
                                                                                                   RCCRYPLTVD FEAFGWDWII
                                                                                                                               LDENGHDLAV
                                                                                                                                                                                     QADGKPKCCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mice by a new TGF-beta
    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IN DEVELOPING AND ADULT
                                                                           CTPTKMSPIN
                                                                                                                                 TFPGPGEDGL
                                                                                                                                                           RSLKLDMSPG
                                                                                                                                                                                     FKFSSKIQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                      FACTOR
                                                                                                                                                                                                                                                                          2293
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II AA_SEQUENCE 1.0

ID GDP8_PIG STANDARD; PRT; 375 AA AC 0.1883;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DT GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (
        GDF8_PAPHA
Sus scrofa (Pig).
Eukaryota; Metazoa;
Eutheria; Cetartioda
                                                                                  GDF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF019619; AAB86686.1; -.
PROSITE; PS00250; TGF_BETA; 1.
PFAM; PF00019; TGF-beta; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM LOSCIE;
TISSUB-SRETEFIAL MUSCLE;
MEDLINE; 98024153.
MCHERRON A.C., LEE S.-J.;
MCHERRON A.C., LEE S.-J.;
"Double muscling in cattle due to mutations in the myostatin ("Double muscling in cattle due to mutations in the myostatin ("Double muscling in cattle due to mutations in the myostatin ("Double muscling in cattle due to mutations in the myostatin ("Double muscling in cattle due to mutations in the myostatin ("Double Regulation of SK "NICLE GROWTH.").

-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                351
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15-JUL-1999
15-JUL-1999
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sanotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Cast annotation update)
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Cast annotation update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last seq
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TISSUE=SKELETAL MU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papio.
                                                                               OR MSTN
                                                                                                                                                                                                                                                                                                             LYFNGKEQII YGKIPAMVVD
                                                                                                                                                                                                                                                                                                                                                               PKRYKANYCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIWQSIDVKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSDGSLEDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRIEAIKIQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MQKLQLCVYI YLFMLIVAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 375
; Metazoa; Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
281
309
313
339
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                         GECEFVFLQK
                                                                                                                                                                                                                                                                                                                                                                                                              PKRSRRDFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLQNWLKQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPVETPTTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHATTETIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSKLRLETAP NISKDAIRQL LPKAPPLREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               February 14, 2000 08:02 Type: P Check: 1463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42688 MW;
                                                                                                                                                                                                                                                                                                             RCGCS
                                                                                                                                                                                                                                                                                                                                                                                                        DCDEHSTESR CCRYPLTVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNLGIEIKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPTESDFLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDLNENSEQK ENVEKEGLCN ACTWRONTKS
                                                                                                                                                                                                                                                                                                                                                         YPHTHLVHQA NPRGSAGPCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQILRLIKPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (BY SIMILARITY)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GROWTH/DIFFERENTIATION FACTOR
GROWTH/ARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61C8D2B7 CRC32;
                                                                                              tation update)
PRECURSOR (GDF-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DENGHDLAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDGTRYTGIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDGKPKCCFF
                                                                                                                                                                                                                                                                                                                                                                                                     EALGWDWIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLKLDMNPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KESSKIQYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDQYDVQRDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPGPGEDGLN
                                                                                                 (MYOSTATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.";
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RRR OCC SOLUTION
                                                                                                                                                                                                                                   IIAA_SEQUENCE 1.0
ID GDF8_RAT
AC 035312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDF8_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF019623; AAB86690.1; --
EMBL; AF019623; AAC808035.1; --
EMBL; AF033795; AAC628035.1; --
EMBL; AF033795; AAC628035.1; --
EMBL; AF033795; AAC628035.1; --
EMBL; AF033795; AAC62809.1; --
EMBL; AF033795; AAC62809.1; --
EMBL; AF03375; AAC62809.1; --
EMBL; AF093795; AAC62809.1; --
EMBL; AF093795; AAC62809.1; --
EMBL; AF09375; AAC62809.1; --
EMBL; AF093795; AAC62809.1; --
EMBL; AA
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SEQUENCE FROM N.A.
TISSUB-SKELETAL MUSCLE;
MEDLINE; 98024153.
MCPHERRON A.C., LEE S.-J.;
MCPHERRON A.C., LEE S.-J.;
Prouble muscling in cattle due to mutations in the myostatin proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8)
GDF8 OR MSTN.
SEQUENCE FROM N.A.
TISSUE=SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                     251
                                                                                                                                                                                                                                                                                                                                                                                                                                               201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUSCLE GROWTH.

-!- SUBCMIT: HOWODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1998)
                                                                                                                                                                                                                                                                                                                        LYFNGKEQII YGKIPAMVVD
                                                                                                                                                                                                                                                                                                                                                               PKRYKANYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                            GIWQSIDVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQKLQIYVYI YLFMLIVAGP VDLNENSEQK ENVEKEGLCN ACMWRQNTKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                     PFLEVKVTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVKAQLWIYL RPVKTPTTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSDGSLEDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRLEAIKIQI LSKLRLETAP NISKDAIRQL LPKAPPLREL
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SEP-1998) to the EMBL/GenBank/DDBJ databases...
NECTS SPECIFICALLY AS A NEGATIVE REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                            GECEFVFLQK
                                                                                                                                                                                                                                                                                                                                                                                                   PKRSRRDFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                            VLQNWLKQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YHATTETIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   February 14, 2000 08:02 Type: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42791 MW;
                                                                                                                                                                                                                                                                                                                        RCGCS
                                                                                                                                                                                                                                                                                                                                                          YPHTHLVHQA
                                                                                                                                                                                                                                                                                                                                                                                                   DCDEHSTESR
                                                                                                                                                                                                                                                                                                                                                                                                                                          SNLGIEIKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQILRLIKPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPTESDLLMQ VEGKPKCCFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                       376
                                                                                                                                                                                                                                                                                                                                                            NPRGSAGPCC
                                                                                                                                                                                                                                                                                                                                                                                                   CCRYPLTVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                            DENGHDLAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDGTRYTGIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDQYDVQRDD
                                                                                                                                              (MYOSTATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Check: 1805
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GDF8_RAT
                                                                  MCPHERRON A.C., LFF C
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DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- F
                                                                                                                                                            Eukaryota; Metazoa;
Eutheria; Cetari
                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN)
                                                                                                                                                                                                                                                                                     SEQUENCE 1.0
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                                                                                                                                                                                             GDF8 OR MS
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"Double muscling in cattle due to mutations in the myostatin gene.";
"Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCPHERRON
                                                               "Double mus
Proc. Natl.
                                                                                                                                                      Caprinae;
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SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY)
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
          SUBUNIT: HOMODIMER, SIMILARITY: BELONGS
                                                HERRON A.C., LEE S.-J.;

uble muscling in cattle due to mutations in the myostatin causeling in cattle acad. Sci. U.S.A. 94:12457-12461(1997).

C. NATL. ACAS SPECIFICALLY AS A NEGATIVE REGULATOR OF SIFUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR.
                                     MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 376
                                                                                                                                                                                                                                                                                                                          MLYFNGKEQI
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                                                                                                                                                         Ovis.
                                                                                                                                                                  Metazoa; Chordata; Craniata;
Cetartiodactyla; Ruminantia;
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376
341
373
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          DISULFIDE-LINKED (BY SIMILARITY).
TO THE TGF-BETA FAMILY.
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Glycoprotein;
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GROWNH/DIFFERENTIATION FACTOR 8
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
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Pecora; Bovoidea; Bovidae;
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                                                    SKELETAL
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!!AA_SEQUENCE
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DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 96029146.
HUANG C.H., XIE S.S., SOCHA W., BLUMENFELD O:O.;
"Sequence diversification and exon inactivation in the gene family from chimpanzee to human.";
J. MOI. EVOL. 41.478-486(1995).
i. FUNCTION: THIS PROTEIN IS A MINOR SIALOGLYCOPROTEIN MEMBRANES.
                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, C)
01-NOV-1997 (Rel. 35, L)
15-JUL-1999 (Rel. 38) L)
GLYCOPHORIN B PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00250, PROSITE; PF00019; TGF-beta; Prowth factor; Cytokine;
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entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                               GYPB OR GPB
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Q28914;
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                                                                                                                             -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE GLYCOPHORIN A FAMILY.
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0; TGF_BETA; 1.
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35, Last sequence update)
38, Last annotation update)
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POTENTIAL.
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POTENTIAL.
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B36084EE CRC32;
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i; Hominidae;
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                                     (See http://www.isb-sib
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le; Pan.
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MBL outstation -
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GPDA_ECOLI Length: 339
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SEQUENCE
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01-OCT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+] (EC 1.1.1.8).
                                                                                                                                                                                           ECOGENE; EG20091; G
PROSITE; PS00957; N
PFAM; PF01210; NAD
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PROSITE; PS00312; GLYCOPHORIN_A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
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PS00957; NAD_G3PDH;
01210; NAD_G1y3P_dh;
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113 P
13246 MW;
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REAALTLLGR ARKDERSSH
                    MDVQSAQEKI GQVVEGYRNT
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BY SIMILARITY.
GLYCOPHORIN B.
POTENTIAL.
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MEDLINE; 96011651.

RAPORT C.J., SCHWEICKART V.L., EI

RAPORT C.J., SCHWEICKART V.L., EI

"The orphan G-protein-coupled rec

related to genes for chemokine re
and neural tissues.";

Gene 163:295-299(1995).
                                                                                                                                                 DOMAIN
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"Cloning, chromosomal localization, and RNA expression of a human beta chemokine receptor 11ke gene.";

DNA Cell Biol. 14:673-680(1995).

"I FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR.";

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

"I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN."

"I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS."

"I SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS."
                                                                  DOMAIN
DISULFID
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TRANSMEM
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DOMAIN
TRANSMEM
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DOMAIN
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                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PFAM; PF00001; 7tm_1; 1.
G-protein coupled receptor; Transmembran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U20350; AAA91783.1;
EMBL; U28934; AAA87032.1;
GCRDB; GCR_1992; -.
GCRDB; GCR_2014; -.
MIM; 601470; -.
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                                                                                                                                                                                                                                                                                                                                                                                                   G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 95374679.
                                                                                                                FRANSMEM
                                                                                                                                 DOMAIN
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Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR13 (V28) (BETA CHEMOKINE RECEPTOR-LIKE 1) (CMK-BRL-1) (CMKBLR1).
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                                                                  d receptor;
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February 14,
                                                40396
                                             MW;
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CYTOPLASMIC (P.
                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane
                                        CYTOPLASMIC (POTENTIAL)
BY SIMILARITY.
; E809E31D CRC32;
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EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
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receptor-encoding gene V28 is closely
e receptors and is expressed in lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Mammalia; i; Hominidae; Homo.
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MDQFPESVTE NFEYDDLAEA CYIGDIVVFG

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LLVVLALTNS

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LLNLALSDLL

FVATLPFWTH YLISHEGLHN

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NFFPSCGMKR CYFRIVETLE VASPQFMFTK

DLRWALSVTE

TVAFSHCCLN IRLILLVVVV

PFIYAFAGEK FFLFWTPYNI SLGVWAAAIL

RKDNECLGDY SCKNRKKARA

PEVLQEIMPV LRNSEVNILG

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GPRD_RAT
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GPRD_RAT
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TRANSMEM
DOMAIN
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HARRISON J.K., BARBER C.M., LYNCH K.R.;

*CONA clonding of a G-protein-coupled receptor (
*CONA clonding of a G-protein-coupled receptor (
*CONA Clonding of a G-protein-coupled receptor (
*CONT ON THE TON THE T
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01-JUN-1994 (Rel. 29, Last seq
01-WOV-1997 (Rel. 35, Last ann
01-WOV-1997 (Rel. 35, Last ann
                                                                                                                                                                                                                                                                                                                                                                        G-protein
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                  TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS002
PFAM; PF00001;
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GCRDB; GCR_0268
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STRAIN-SPRAGUE-DAV
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: MOST ABUNDANT IN ADULT SPINAL CORD, E
KIDNEY, GUT, UTERUS AND TESTES.
PTM: THIS PROTEIN TO YOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: THIS PROTEIN IS NOT N-GLYCOSYLATED WHICH IS UNUSUAL G-PROTEIN-COUPLED RECEPTORS.
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                                                                                                                       1 receptor;
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annotation update)
RECEPTOR GPR13 (RBS11).
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CYTOPLASMIC (POTENTIAL)
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Rattus.
         Check: 4478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRUNET J.F., DÖSSETO M., DENIZOT F., M
HAQQI T.M., FERRIER P., NABHOLZ M., SC
LUCIANI M.F., GOLSTEIN P.;
"The inducible cytotoxic T-lymphocyte-
CTLA-1 sequence and gene localization
Nature 322:268-271(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-UL-199 (Rel. 38, Last annotation update)
15-UL-199 (Rel. 38, Last annotation update)
GRANIZME B(G,H) PRECURSOR (EC 3.4.21.79) (CYTOTOXIC CELL PROTEASE
(CCP1) (CTLA-1) (FRAGMENTIN 2).
CZMB OR CTLA-1 OR CTLA-1.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 94319082.

KO M.S., WANG X., HORTON J.H., HAGE MAEZAKI Y., NADEAU J.H.;

"Genetic mapping of 40 cDNA clones Mamm. Genome 5:349-355(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILINE; 89062424., DUGGAN B., EHRMAN N., LET

LOBE C.G., UPTON C., DUGGAN B., EHRMAN N., LET

MCFADDEN G., BLEACKLEY R.C.;

"Organization of two genes encoding cytotoxic

serine proteases CCPI and CCPII.";

Biochemistry 27:6941-6946(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
D-STRUCTURE MODELING.
MEDILINE; 89184501.
MURCHY M. E.P., MOULT J., BLEACKLEY R.C.,
MURCHY M. I.I., JAMES M.N.G.;
"Comparative molecular model building of
cytotoxic T lymphocytes.";
                                                                                                                                                                                                                           SEQUENCE OF 21-40.
MEDLINE, 87215932
MASSON D. TSCHOPP J.;
"A family of serine esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 86208120.

LOBE C.G., FINLAY B.B., PARANCHYCH
NOVel serine proteases encoded by
ymphocyte-specific genes.";
science 232:858-861(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 227-247 FROM N.A.
                                                                                                                                                                               lī 49:679-685(1987).
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to mouse chromosome 14.";
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cytotoxic
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                                   serine
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Mus.
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GRAB_MOUSE Length:
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P50270
                                                                                                                                                                                                      _SEQUENCE 1.0
HDHA_CLOSO
7-DEHILL SOLUCION COLOR FIRMICULES;
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DISULFID
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SEQUENCE
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DISULFID
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its
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SIGNAL
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LL; M12302; AAA37383.1;

SL; M25526; AAB61756.1;

SL; U05707; AAB60470.1;

SL; U05707; PRMSCL.

SL; A28952; A28952,

SL; A28952; A28952,

SL; A28952; A28952,

SL; A26944; B26944.
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CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ASP-|-XAA >> AS-
MET-|-XAA, SER-|-XAA.

SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES OF CYTOLYTIC T-
LYMPHOCYTES AND NATURAL KILLER CELLS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
TRYPSIN FAMILY. STRONGEST TO OTHER GRANZIMES AND TO MAST O
PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        teins 4:190-204(1988).

FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-MEDIATED IMMUNE RESPONSES. IT CLEAVES AFTER ASP. SEEMS TO BE LINKED TO AN ACTIVATION CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES CASPASE-3, -7, -9 AND 10' TO GIVE RISE TO ACTIVE ENZYMES MEDIATING
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                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                     QEVELTVQKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182
27470 MW;
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GRANZYME B(G,H).

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(EC 1.1.1.159)
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               group;
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SIMILARITY).
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            SEQUENCE FROM N.A.
MEDLINE: 84207945.
STRUBIN M., MACH B., LONG
"The complete sequence of
invariant chain reveals a
                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 86093681.
KUDO J. CHAO L.Y., NARNI F., SAUNDERS (
"Structure of the human gene encoding the class II histocompatibility antigens.";
Nucleic Acids Res. 13:8827-8841(1985).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                      P04233; Q29832;
20-MAR-1987 (Rel. 04, Created)
01-JUL-1933 (Rel. 26, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CH
ASSOCIATED INVARIANT CHAIN) (P33) (CD74 ANTIGEN).
CD74 OR DHLAG.
                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1.0
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SEQUENCE
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HSSP; P25529; IAHH.
PROSITE; PS00061; ADM_SHORT; 1.
PFAM; PF00106; adh_short; 1.
PFAM; PF00678; adh_short_C2; 1.
Oxidoreductase; NADP; Bile acid catabolism.
NP_BIND 10 34
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hydroxysteroid dehydrogenase gene from Clostridium sordelili.";
J. Bacteriol. 176:4665-4874(1994).
'- CATALYIC ACTIVITY: 3-ALPHA, 7-ALPHA, 12-ALPHA-TRIHYDROXY-5-BETA-
CHOLANATE + NADP(+) - 3-ALPHA, 12-ALPHA-DIHYDROXY-7-OXO-5-BETA-
CHOLANATE + NADPH.
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INDUCTION: BY BILE ACID. EXPRESSED DURING GROWTH-PHASE.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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267 AA;
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29177 MW;
LONG E.O.;
ce of the mRNA for the
als a polypeptide with
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         HLA-DR-associated an unusual transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Type:
            unusual transmembrane
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[4]
SEQUENCE FROM N.A.
MEDLINE; 86233451.
~'entilivan D.M., Larhammar D., Wilson M.C., Peterson P.A.,
-'entilivan D.M., Larhammar D., Wilson M.C., Peterson P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLAESSON L., LARHAMMAR D., RASK L., "cDNA clone for the human invariant histocompatibility antigens and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                        JASANOFE A. WAGNER G., WILEY D.C.;

JASANOFE A. WAGNER G., WILEY D.C.;

Structure of a trimeric domain of the MHC class II-associated chaperonin and targeting protein II.";

EMBO J. 17.6812-6818(1998).

- PROCTION: PLAYS A CRITICAL ROLE IN MHC CLASS II ANTIGEN PROCESSING PROCESSING PROMOTICS. FREE CLASS II ALPHA/BETA HETERODIMERS IN A COMPLEX SOON AFTER THEIR SYNTHESIS AND DIRECTING TRANSPORT OF THE COMPLEX FROM THE ENDOPLASMIC RETICULM TO COMPARTMENIS WHERE PEPTIDE LOADING OF CLASS II TAKES PLACE.

- PEPTIDE LOADING OF CLASS II TAKES PLACE.

- PEPTIDE LOADING OF CLASS II TAKES PLACE.

- PEPTIDE LOADING OF CLASS II THE ALPHA/BETA/GAMMA HETEROTRIMERS.

- SUBUNT: NONAMER COMPOSED OF THEE ALPHA/BETA/GAMMA HETEROTRIMERS.

- SUBULTARITY: CONTAINS I THYROGLOBULIN TYPE-I DOMAIN.

- SINILARITY: CONTAINS I THYROGLOBULIN TYPE-I DOMAIN.

- PATABASE: NAME-PROW; NOTE-CD Guide CD74 entry.

- WWM-"http://www.ncbi.nlm.nih.gov/prow/cd/cd71.htm".
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EMBO J. 3:869-872(1984).
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatis the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHOSH P., AMAYA M., MELLINS E., WI "The structure of an intermediate bound to HLA-DR3."; hature 378:457-462(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structure
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                                                            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                    PROSITE; PS00484; THYROGLOBULIN_1; 1.

PFAM; PF00086; thyroglobulin_1; 1.

Glycoprotein; MHC; Proteoglycan; Transmembrane; Alternative
                                                                                                                                                                                                                                                   EMBL; X03339; CAA27046.1; --
EMBL; X03340; CAA27047.1; --
EMBL; X01144; AAA36304.1; --
EMBL; X00497; CAA25192.1; --
EMBL; X00497; CAA25193.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structure of the human Ia-associated dentification of 5' sequences shared
                                                                                                                                                                                                       PIR; A30060; HLHUG.
PDB; 1A6A; 27-MAY-98.
PDB; 1IIE; 15-FEB-99.
                                                                                                                                                                                    1IIE; 1
142790;
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Natl. Acad. Sci. U.S.A.
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   47
103
136
136
282
                                                                                                                             3D-structure
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                                                              CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
CLIP.
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   GLYCOSAMINOGLYCAN. THYROGLOBULIN TYPE
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gamma chain of class
implications for the
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with major histocompatibility
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                                                                                                                                                                                        EMBL; X13464; CAA31824.1; ...
EMBL; J01804; AAA88616.1; -..
PIR, JS0158; XNEBHC.
STYGENE; SG10159; HISC.
PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
PFAM; PF00222; aminotran_2; 1.
PFAM; PF00222; aminotran_2; 1.
PYRIDOXAL PIPIIOXAL PIPIIOX
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CONFLICT
SEQUENCE
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01-AUG-1992 (Rel. 23, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-
PHOSPHATE TRANSAMINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BARNES W.M., HUSSON R.N., WHITTIER R.;

Submitted (AUG-1989) to the EMBL/Genbank/DDBJ databases.

1. CATALYTIC ACTIVITY: L-HISTIDINOL-PHOSPHATE + 2-OXOGLUTARATE = 3-(IMLDAZOL-4-YL)-2-OXOGROPYL PHOSPHATE + GLUTAMATE.

1. COFACTOR: PYRIDOXAL PHOSPHATE.

1. PATHWAY: EIGHTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.

1. SUBUNIT: HOMODIMER.

1. SUBUNIT: HOMODIMER.

1. SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CARLOMAGNO M.S., CHIARIOTTI L., ALIFANO P., NAPPO A.G., BRUNI C.B.; Carlomagno m.S., Chiariottichia "Structure and function of the Salmonella typhimurium and Escherichia coli K-12 histidine operons.";

J. Mol. Biol. 203:585-606(1988).
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Bacteria; Proteobacteria;
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(IN REF. 2).
C -> R (IN REF. 1).
L -> S (IN REF. 1).
GI -> ES (IN REF. 1).
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01-CCT-1996 (Rel. 34, Creat
01-NOV-1997 (Rel. 35, Last
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HISTIDINE TRANSPORT SYSTEM
                                                                                                                                                                                                                                                                                                       MEDLINE; 97426617.

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BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BUBLATINER F.R., PLOULABO-VIDES J., GLASNER F.D., RODE C.K., MAYHI GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSI MAU B., SHAO Y.;

MAU B., SHAO Y.;

"The complete genome sequence of Escherichia coli K-12.";

science 277:1453-1474(1997).
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S.J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
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HISQ_ECOLI Length: 228
                                                                                         "PCR cloning expressed in
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EMBL; AE000319;
EMBL; D90862; CP
                                                                                                                                                                                                                   HOMEDBUA FROM HEX.
PRHX OR PRH OR HEX.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1995 (Rel. 32, Last annotation update)
HOMEOBOX_PROTEIN PRH (HOMEOBOX PROTEIN HEX).
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TRANSMEM
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TRANSMEM
MEDLINE, 93219088.

BEDFORD F.K., ASHWORTH A., ENVER T., WEDTORD F.K., ASHWORTH A., ENVER T., WEDTOR TOWN GENE EXPRESSED CONSERVED BY THE METERS OF T
                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 93087175.

CROMEPTON M.R., BARGLETT T.J., MACGREGOR A.D., MANFIOLETTI
CROMEPTON M.R., GIANCOTTI V., GOODWIN G.H.;

"Identification of a novel vertebrate homeobox gene expres
haematopoletic cells.";

Nucleic Acids Res. 20:5661-5667(1992).
                                                                                                                                                                                                                                                                                                                                                             201
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PROSITE; PS00402; BPD_TRANSP_INN_MEMBR;
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                                                                                                                       MEDLINE; 93384629.
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                                                             EQUENCE OF 122-270 FROM N.A.
                                                                                  iochem.
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                                                                               .A., COLLINS S.J., RADICH J.;
ning of an orphan homeobox gene (PRH) preferentially
d in myeloid and liver cells.";
Biophys. Res. Commun. 195:976-983(1993).
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34
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109
173
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CAB22089.1;
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PERICLASMIC (POTENTIAL).
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V -> C (IN REF. 1).

D -> Y (IN REF. 1).

I -> M (IN REF. 1).

G -> C (IN REF. 1).

P -> A (IN REF. 1).

VF -> MC (IN REF. 1).

VF -> MC (IN REF. 1).
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CYTOPLASMIC (POTENTIAL)
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                                          WIEDEMANN L.M.;
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                              during haematopoiesis
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HMPH_HUMAN Length:
                                      SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-EMBRYO;

STRAIN-C59BL/6J; TISSUE-EMBRYO;

MEDLINE; 9321908.

MED
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                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995
01-NOV-1995
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1
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EMBL; L16499; AAA02988.1; -.
EMBL; Z21533; CAA79730.1; -.
PIR; S26799; S26799.
                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1. PFAM; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence upo
01-NOV-1997 (Rel. 35, Last annotation upo
HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: EXPRESSED DURING HEMATOPOIESIS.
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FUNCTION: RECOGNIZES THE DNA SEQUENCE 5'-ATTAA-3'. MP
IN HEMATOPOIETIC DIFFERENTIATION.
SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
TISSUB SPECIFICITY: LIVER AND PROMYELOCYTIC LEUKEMIA
LINE HL60.
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DNA-binding; Developmental
1 133 PRO-RIC
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345:93-88(1994).
N: RECOGNT""
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115 L -> V (IN REF. 2).
30021 MW; 453E9E6A CRC32;
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d during haematopoiesis
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HMPH_MOUSE
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HPRK_BACSU
034483;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Bactilus subtilis.
Bactilus Firmicutes; Bacillus/Clostridium
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                 MEDILNE; 98230327.
REIZER J., HOISCHEN C., TITGEMEYER F., RIVOLTA C., STUBLKE J., KARAMATA D., SAIER M.H. JR., HILLEN W. "A novel protein kinase that controls carbon catab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                MEDILINE: 99141583.

KRAVANJA M., ENGELMANN R., DOSSONNET V., BLUGGEL M., MEYER H.E., FRANK R., GALINIER A., DEUTSCHER J., SCHNELL N., HENGSTENBERG W.;

"The hprk gene of Enterococcus faecalis encodes a novel bifunctional harmonic the HPr kinase/phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
LAZAREVIC V., SOLDO B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
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PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS50071; HOMEOBOX_2;
PFAM; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                    CHARACTERIZATION, MEDLINE; 98230327
                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i5-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HPR(SER) KINASE/PHOSPHATASE (EC 2.7.1.-) (EC
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yme: the HPT kinase/phosphatase.";
Microbiol. 31:59-66(1999).
Microbiol. 31:59-66(1999).
FUNCTION: THIS KINASE/PHOSPHATASE REGULATES CARBOHYDRATE UPTAKE AND METABOLISM BY PHOSPHORYLATING/DEPHOSPHORYLATING SER-45 OF THE PHOSPHORYL CARRIER PROTEIN (HPR) OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS) IN RESPONSE TO CYTOPLASMIC METABOLITE LEVELS AS A DEVICE FOR THE MODULATION OF CARBON CATABOLITE REPRESSION.

ENZYME REGULATION: ALLOSTERICALLY ACTIVATED BY METABOLITES SUCH AS
                                                                                                                                                                                                                            Microbiol.
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271 AA;
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FRUCTOSE-1,6-BISPHOSPHATE AND INHIBITED BY INORGANIC PHOSPHATE MASS SPECTROMETRY: MW-34529; METHOD-MALDI.
SIMILARITY: BELONGS TO THE PTSK FAMILY.

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ALD PROPERTY OF THE PROPERTY O
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ID HUPK_RHILV
AC P28153;
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                              SCHMITT H
                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE; 95020662.

IMPERIAL J., REY L., RUIZ-ARGUESO T.;

"Hupk, a hydrogenase-ancillary protein from Rhizobium leguminosarum, shares structural motifs with the large subunit of NiFe hydrogenases and could be a scaffolding protein for hydrogenase metal cofactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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MEDILINE; 93106466.

REY L., HIDALGO E., PALACIOS J.M., RUIZ-ARGUESO T.;

"Nucleotide sequence and organization of an H2-uptake gene cluster from Rhizobium leguminosarum bv. viciae containing a rubredoxin-like gene and four additional open reading frames.";

J. Mol. Biol. 228:998-1002(1992).
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NP_BIND
NP_BIND
SEQUENCE
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Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
01-MOV-1997 (Rel. 35, Last annotation HUPK.
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EMBL; Z99121; CAB15505.1; -.
SUBTILIST; BG14125; PTSK.
Multifunctional enzyme; Transferase; Serine/threonine-protein kinase;
ATP-binding; Hydrolase.
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LOTZ W.;
(SEP-1994) to
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152
309 AA;
                                                  KOKOTEK W.,
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159
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  the EMBL/GenBank/DDBJ databases
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subdivision;
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                                            BAUER T.,
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!!AA_SEQUENCE 1.0
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                           SEQUENCE FROM N.A.
STRAIJ=K12 / M01655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SENOY.;
MAU B., SENOY.;
                                                                                                                                                                                                                                                                                                                   HYCD OR HEVD.
Escherichia co
Bacteria; Pro
Escherichia.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / MC4100;
MEDLINE; 90251163,
BOEHM R., SAUTER M., BOECK A.;
Nucleotide sequence and expression
coding for formate hydrogenlyase com
nol Microbiol 4:231-243(1990).
                                                                                                                                                                                                                                                                                                                                                                  P16430;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
FORMATE HYDROGENLYASE SUBUNIT 4 (FHL SUBUNIT
                                                                                                                                                                                                                                                                                                                                                              COMPONENT
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SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the En
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Z36981; CAA85440.1; -.
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CRC32;
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AE1R; S08622;

BECOGENE; EGIL

DR PROSITE; PS006

R PFAM; PF00146; N.

OXIGOREDUCTASE; T.

TRANSMEM 8

TRANSMEM 94 11

NANSMEM 132 152

VSMEM 168 188

VMM 285

VEM 254 274

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VM 307 p.
  HYCD_ECOLI
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SEQUENCE.

MARDA K., WARKBAYASHI S., MATSUBARA H.;

MAEDA K., WARKBAYASHI S., MATSUBARA H.;

MAEDA K., WARKBAYASHI S., MATSUBARA H.;

MAEDA M.;

MAEDA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ALPHA-AMYLASE INHIBITOR 0.19 (0.19 AI) (0.19 ALPHA-AI).
Triticum aestivum (Wheat). 19 (0.19 AI) Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales; Paaceae; Triticum.
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                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE-KERNEL; OKUDA M., SATOH T.
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                                                                                                                                                      OKUDA M., SATOH T., SAKURAI N., SHIBUYA K., KAJI H., SAMEJIMA "Overexpression in Escherichia coli of chemically synthesized active 0.19 alpha-amylase inhibitor from wheat kernel."; J. Biochem. 122:918-926(1997).
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MEDLINE; 98022743... FUKUYAMA K., MIYAZAKI T., MORIMOTO T.; ODA Y., MATSUMAGA T., FUKUYAMA K., MIYAZAKI T., MORIMOTO T.; "Tertiary and quaternary structures of 0.19 alpha-amylase inhibitor from wheat kernel determined by X-ray analysis at 2.06-A resolution.";
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                                                                                       X-RAY CRYSTALLOGRAPHY MEDLINE; 98022743.
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ITE; PS00667; COMPLEX1_ND1_1; 1

ITE; PS00668; COMPLEX1_ND1_2; 1

I; PF00146; NADHdh; 1.

Ioreductase; Transmembrane; Inne
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IIAA_SEQUENCE 1.0
IIAA_WHEAT
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AC POIO83;
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PDB; 1HSS; 01-JUL-98

PROSITE; PS00426; CEREAL_TRYP_AMYL_INH; 1.

PFAM; PF00234; tryp_alpha_amyl; 1.

Alpha-amylase inhibitor; Multigene family; Se
DISULFID 6 52
DISULFID 20 41
DISULFID 28 83
DISULFID 28 83
DISULFID 42 99
DISULFID 54 115
SEQUENCE 124 AA; 13337 MM; 05CA1F5D.CRC32
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01-AUG-1991 (Rel. 19, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
ALPHA-AMYLASE INHIBITOR 0.28 (CIII) (WMAI-1).
Tritt.cum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
     MEDLINE; 92032760.

GARCIA-MAROTO F., CARBONERO P., GARCIA-OLMEDO F.;

GARCIA-MAROTO F., CARBONERO P., GARCIA-OLMEDO F.;

GARCIA-MAROTO F., CARBONERO P., GARCIA-OLMEDO F.;

WMAI-L, a wheat monomeric inhibitor of insect alpha-amylase.";

Plant Mol. Biol. 17:1005-1011(1991).

-!- FUNCTION: ALPHA-ANYLASE INHIBITOR.

-!- SUBUNIT: MONOMER.

-!- TISSUE SPECIFICITY: ENDOSPERM.
                                                                                                                                                                                                                                                      STRAIN-CV. PASTORE;

MEDLINE; 9.3309.10.

POERIO E., CAPPRALE C., CARRANO L., PUCCI P., BUONOCORE V.;

PASSIGNMENT of the five disulfide bridges in an alpha-amylase inhibitor from wheat kernel by fast-atom-bombardment mass spectrometry and Edman degradation.";

Spectrometry and Edman degradation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.

KASHLAN N., RICHARDSON M.

"The complete amino acid
of alpha-amylase.";
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HSSP; P01085; 1HSS.

PROSITE; PS00426; CEREAL\_TRYP\_AMYL\_INH; 1.
PFAM; PF00234; tryp\_alpha\_amyl; 1.
Alpha-amylase inhibitor; Multigene family; Seed.
DISULFID 7

; WIWTA.

PTM: THE DISULFIDE BONDS ARE ESSENTIAL FOR THE INHIBITOR ACTIVITY SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INHIBITOR FAMILY.

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S -> A (IN 50% OF THE MOLECULES).
Y -> A (IN VERY SMALL AMOUNT).
CK -> GP (IN VERY SMALL AMOUNT).
A -> C (IN REF. 1).
82F56DD7 CRC32;

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R PROSTE; PO1085; HIST.

R PROSTE; PS00426; CEREAL_TRYP_AMYL_INH; 1.

R PEAM; PE00234; tryp_alpha_amyl; 1.

M Alpha-amylase inhibitor; Multigene family; S
T DISULFID 6 115
T DISULFID 20 41 OR 20-42.
FT DISULFID 20 83
DISULFID 42 99 OR 41-99.
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                                                                                                                                                                                                              MEDLINE; 84061717.

MAEDA K., WAKABAYASHI S., MATSUBARA H.;

"Disulfide bridges in an alpha-amylase inhibitor from wheat kernel.";

J. Blochem. 94.865-870(1993).

-I- FUNCTION: ALPHA-AMYLASE INHIBITOR.
                                                                                                                                                                                                                                                                                                                   REVISIONS TO 119-124.

REVISIONS TO 119-124.

MAEDLINE; 85175148.

MAEDDA K., WAKNABYASHI S., MATSUBARA H.;

"Complete amino acid sequence of an alpha-amylase kernel (0.19-inhibitor),";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
ALPHA-AMYLASE INHIBITOR 0.53.
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                        -!- SUBUNIT: HOMODIMER.
-!- TISSUE SPECIFICITY: ENDOSPERM.
-!- TISSUE SPECIFICITY: EONDS ARE ESSENTIAL FOR THE INHIBITOR ACTIVITY.
-!- PTM: THE DISULETIDE BONDS ARE ESSENTIAL FOR THE INHIBITOR ACTIVITY.
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MAEDA K., HASE T., MATSUBARA H.;
"Complete amino acid sequence of an alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                           kernel.";
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267 210

CASPASE-2 SUBUNIT 1 CASPASE-2 SUBUNIT 2 BY SIMILARITY.

(BY

SIMILARITY)

Hydrolase;

protease; 266 >312 210

Apoptosis;

Zymogen.

PFAM;

PF00619; CARD; 1. PF00655; ICE\_P10; PF00656; ICE\_P20;

EMBL; AF025671; AAB82567.1; -.
EMBL; U34684; AAC52260.1; -.
HSSP; P29466; 1IBC.
PROSITE; PS01121; CASPASE\_HIS;
PROSITE; PS01122; CASPASE\_CYS;

restrictions

in

no on

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!!AA_SEQUENCE 1.0

ID ICE2_RAT

AC P55215; 035398;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-UT1-1998 (Rel. 36, Last sequence update)

DT 15-UT1-1998 (Rel. 38, Last annotation update)

DT 15-UT1-1998 (Rel. 38, Last annotation update)

DE CASPASE-2 PRECURSOR (EC 3.4.22.-) (CASP-2) (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-257 FROM N.A.
TISSUE-KIDNEY CORTEX;
MEDLINE; 98191309.
MEDLINE; 98191309.
"Identification of gene family of caspases in expression in ischemia-reperfusion injury.";
am. J. Physiol. 274:F587-F595(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96042508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-OVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 131-312 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CASP2 OR ICH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                              PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPERTIDE, BUT NO THAT OF OTHER CASPASES (BY SIMILARITY).

SIMILARITY: BELONGS TO PERTIDASE FAMILY C14; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                       CASPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPIVVDASGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   February 14, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13185 MW;
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Rattus.
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Check:

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KGGSFSQNVE

LLNLLPKRGP QAFDAFCEAL

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IIAA_SEQUENCE 1
ICW3_PSOTE
AC p10822;
AC p20822;
AC p20
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01-JUL-1991 (Rel. 19, Last sequence update)
15-JUL-1992 (Rel. 38, Last annotation update)
15-JUL-1992 (Rel. 38, Last annotation update)
CHYMOTRYPSIN INHIBITOR 3 PRECURSOR (WCI-3).
Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                     SHIBATA H., HARA S., IKENAKA T.;

"Amino acid sequence of winged bean (Psophocarpus tetragonolobus DC.) chymotrypsin inhibitor, WCI-3.";

DC.) chymotrypsin inhibitor, WCI-3.";

J. Biochem. 104:537-543(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 94122379.
HABU Y., SAKATA Y., FUKASAWA K., OHNO T.;
"Ubiquitous nuclear proteins bind to 5' upstream x
"Ubiquitous nuclear proteins bind to 5' upstream x
Kunitz chymotrypsin inhibitor gene in winged bean.
Kunitz chymotrypsin inhibitor gene in winged bean.
Flant Mol. Biol. 23:1139-1150(1993).
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PEYACHOKNAGUL S., MATSUI T., SHIBATA H., HARA S., IKENAKA T.,

OKADA Y., OHNO T.;

Sequence and expression of the mRNA encoding the chymotrypsin

inhibitor in winged bean (Psophocarpus tetragonolobus (L.) DC.).";

plant Mol. Biol. 12:51-58(1989).
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      X-RAY CRYSTALLOGRAPHY
MEDLINE; 99258819.
DATTAGUPTA J.K., PODDE
DUTTA S.K., SINGH M.;
                                                                                                                                 "Structure of a Kunitz-Type 2.95-A resolution."; Acta Crystallogr. D 52:521-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 92234991.
                                                                                                                                                                                                                          SINGH M.;
                                                                                                                                                                                                                                                                              TISSUE-SEED;
                                                                                                                                                                                                                                            DATTAGUPTA J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HABU Y., PEYACHOKNAGUL S., UMEMOTO K., SAKATA Y., OHNO T.; "Structure and regulated expression of Kunitz chymotrypsin inhibitor genes in winged bean [Psophocarpus tetragonolobus (L.) DC.]."; "Biochem. 111:249-258(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDLINE; 89197853.
                                                                                                                                                                                                                                                                                                    -RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS)
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         PODDER
H M.;
                                                                                                                                                                                                                                               PODDER A.,
                                                                                                                                          52:521-528(1996).
                                                                                      (2.3
                                 A.,
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                                                                                                                                                                                        chymotrypsin
                                 CHAKRABARTI
                                                                                                                                                                                                                                                  CHAKRABARTI C.,
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SEQUENCE 1.0

201

SETASSH

STRAIN=H37RV;
MEDLINE; 98295987.
COLE S.T., BROSCH R., 1
GORDON S.V., EIGLMEIER

PARKHILL R K., GAS

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GARNIER BARRY C.

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CHURCHER C

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SEQUENCE

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F72002; 008150;

15-DEC-1999 (Rel. 39, Created)

15-DEC-1999 (Rel. 39, Last sequence update)

15-DEC-1999 (Rel. 39, Last annotation update)

PUTATIVE ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (EC 5.3.3.2) (IPP ISOMERASE) (ISOPENTENYL PYROPHOSPHATE ISOMERASE).

RV1745C OR MTCY28.08C OR MTCY04C12.29C.

Mycobacterium tuberculosis.

Bacteria; Firmlcutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmlcutes; Actinobacteria; Mycobacterium.

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SETTITIVE DESERVATION DE LA RESERVATION DE LA RE
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                                                                                                                                                                                                                                                                                                                                                                          Serine protease inhibitor; S
SIGNAL 1 24
CHAIN 25 207
DISULFID 65 109
DISULFID 159 168
ACT_SITE 89 90
SEQUENCE 207 AA; 22774 MW
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DISULFID
DISULFID
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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"2.13-A structure of a Kunitz-type winged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Refined crystal structure (2.3 A) of a double-headed winged bean alpha-chymotrypsin inhibitor and location of its second reactive site.";
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151
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PFAM; PF00197; Kunitz_legume; 1.
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BL; D13974; BAA03084.1; -.
BL; D13975; BAA03086.1; -.
BL; D13976; BAA03086.1; -.
BL; D13976; BAA03086.1; -.
BL; D13976; BAA03086.1; -.
BAD03086.1; -.
BAD03086.
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FUNCTION: INHIBITS ALPHA-CHYMOTRYPSIN AT THE MOLAR RATI
IN STATE OF 1:1.
SIMILARITY: TO OTHER LEGUMINOUS KUNITZ-TYPE INHIBITORS.
IHVYKLLYCQ
                                                                      LGFANPPSCA
                                                                                                                                                      HGGGIETAKT
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207
207
168
90
22774 MW;
                                                                           ASPWWTVVDS
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HDEEDVKCDQ
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    YIGIHRDRNG
                                                                           PQGPAVKLSQ
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                                                                                                                                                          RSPNEVSKGE
                                                                                                                                                                                                                                 SSTADDDLVD AEGNLVENGG
                                                                                                                                                                                                                                                                                                                                                                                   REACTIVE BOND (CHYMOTRYPSIN); 22B8B770 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHYMOTRYPSIN INHIBITOR
                                                                           QKLPEKDILV FKFEKVSHSN
    NRRLVVTEEN
                                                                                                                                                          PIRISSOFLS
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        PLELVLLKAK
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIR-K12 / MG1655;
MEDLINE; 9533436;
BURLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995
01-FEB-1995
15-DEC-1999
"Sequence analysis of the GntII (subsidiary) system for gluconate metabolism reveals a novel pathway for L-idonic acid catabolism in Escherichia coll."

J. Bacteriol. 180:3704-3710(1998).

-i- FUNCTION: IDN OPERON REGULATOR. MAY REPRESS GNTKU AND GNTT GENIWHEN GROWING ON L-IDONATE.
                                                                                                  BAUSCH C.,
CONWAY T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HONSBY T., JAGELS K., KROCH A., MCLEAN J., MOULES S., MERHY L., OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E. TAYLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).

11- FUNCTION: CATALYZES THE 1,3-ALLYLIC REARRANGEMENT OF THE
                                                                                                                                                                                 "Annalysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                       Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
ACT_SITE 75 7
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|-FEB-1995 (Rel. 31, Last sequence update)
|5-DEC-1999 (Rel. 39, Last annotation update)
|-IDONATE REGULATORY PROTEIN.
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203 AA;
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BY SIMILARITY.

4 BY SIMILARITY.

2489 MW; 4D4FFD37 CRC32;
                                                                                                                 UTZ C.,
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                                                                                                               BLAIS T.,
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                                                                                                               MURRAY E.,
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A LO COCCO C

AND GNTT GENES

Bacteriocin; Colicin;

124 15245 MW;

POTENT

BA839D94 CRC32;

POTENTIAL.

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!!AA_SEQUENCE 1.0
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Plasmid ColN pCHAP4.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY
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PROSITE; PS00356; HTH_LACI_FAMILY; 1.

PFAM; PF00356; Hoc; 1.

PFAM; PF00532; Peripla_BP_like; 1.

Transcription regulation; DNA-binding; Gluconate utilization.

DNA_BIND

8 27

H-T-H MOTIF (POTENTIAL).

SEQUENCE 332 AA; 37567 MW; B4E1F229 CRC32;
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 8817
PUGSLEY A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as low
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EMBL; x06933; CAA30020.1; -. PIR; S01761; IMECN4. Plasmid; Bacteriocin; Colici
                                                                                                                                                                                                                                                                                                             "The immunity and lysis genes of ColN plasmid pCHAP4."; Mol. Gen. Genet. 211:335-341(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Pr
Escherichia.
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EMBL; AE000497; AAC77221.1;
HSSP; P03023; 1LCD.
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IMMN\_ECOLI

Length:

131

February

14,

2000 08:02

Type: P

Check: 6528

MHNTLLEKII

AYLSLPGFHS

LNNPPLSEAF NLYVHTAPLA ATSLFIFTHK

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IIAA_SEQUENCE 1.0
ID IPRA_SAGSA
AC P31608;
DT 01-UUL-1993 (F
DT 01-UUL-1993 (F
DT 01-OCT 1993 (F
DE PROTEINASE INE
DE A) (API-A)
OS Sagittaria sag
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01-NOV-1990 (Rel. 1
01-NOV-1990 (Rel. 1
15-DEC-1998 (Rel. 3
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"DNA sequence analysis of the imp UV protection and mu of the plasmid TPII0: identification of a third gene." Nucleic Acids Res. 18:5045-5050(1990).

"INCLUSED IN UV PROTECTION AND MUTATION." SIMILARITY: BELONGS TO THE IMPB/MCCB/SAMB FAMILY.

"ISMILARITY: BELONGS TO THE IMPB/MCCB/SAMB FAMILY."
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                        IPRA_SAGSA STANDARD; PRT; 181 AA.

P31608;

01-JUL-1993 (Rel. 25, Created)

01-JUL-1993 (Rel. 27, Last sequence update)

01-OCT-1993 (Rel. 27, Last annotation update)

PROTEINASE INHIBITOR A PRECURSOR (DOUBLE-HEADED PROTEINASE INHIBITOR
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Plasmid IncIl TP110.
Bacteria; Proteobacteria;
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PFAM; PF00817; IMS;
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    Sagittaria sagittifolia (Arrowhead).
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424 AA; 47786 MW; FE14F2F4 CRC32;
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37,
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SEQUENCE OF 25-174.

WANG H.-L., LUO R.-S., WANG L.-
"Primary structure and disulfid headed proteinase inhibitors.";

J. Biochem. 111:537-545(1992).

-i- FUNCTION: POSZESZEST TWO REF.

AMOUNT OF TRYPSIN AND CHYMO
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ACT_SITE
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XU W., T.
                                                                                              IS12_STRAL STANDARD; PRT; 256 AA. P23393; P23393; Ol-NOV-1991 (Rel. 20, Created) Ol-NOV-1991 (Rel. 20, Last sequence update) Ol-NOV-1991 (Rel. 20, Last annotation update) INSERTION ELEMIN IS112 28.4 KD PROTEIN.
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-i- SIMILARITY: STRONG, TO S.SAGITTIFOLIA PROTEINASE INHIBITORS B.
SEQUENCE FROM N.A. MEDLINE; 9115926.
RODICIO M.R., ALVAREZ M.A., CHATE TOUTION and genetic structure responsible for the inactivation
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                                                                   Streptomyces albus 9.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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IS12_STRAL Length: 256 February 14, 2000
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1. INDUCTION: BY IRON STRESS."
EMBL; L26530; AAA27291.1; -. EMBL; D90910; BAA17948.1; -. PFAM; PF00421; PSII; 2. Photosystem II; Chlorophyll; TRANSMEM 30 51
                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q55274; P73884;
Q55274; P73884;
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 36, Last annotation update)
L5-JUL-1998 (Rel. 36, Last annotation update)
LFON-STRESS INDUCED CHLOROPHYLL-BINDING PROTEIN.
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SEQUENCE FROM N.A.
FERREIRA F., STRAUS N.A.;
FERREIRA F., FORC-1993) to t
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MO1. Gen. Genet. 225:142-147(1991).
-!- FUNCTION: INACTIVATION OF SAL I RESTRICTION-MODIFICATION SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLINE; 97061201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).

-!- CATALYTIC ACTIVITY: 2-DEOXY-D-GLUCONATE + NAD(+) = 3-DEHYDRO-2-DEOXY-D-GLUCONATE + NADH.

-!- PATHWAX: PECTIN DEGRADATION.

-!- PATHWAX: PECTIN DEGRADATION.

-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

FAMILY (SDR).
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Oxidoreductase; NAD.
NP_BIND 16
ACT_SITE 159 1
SEQUENCE 254 AA;
                                                                                                                                          EMBL; L47838; AAB38476.1; --
EMBL; Z99115; CAB14131.1; --
HSSP; P19992; ZHSD.
SUBTILIST; BG11400; KDUD.
SUBTILIST; BG11400; KDUD.
SPROSITE; PS00061; ADH_SHORT;
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STRAIN-168 / MARBURG;
MEDLINE; 96349105.
SOROKIN A.V., AZEVEDO V.,
SERBOR
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
2-DEOXY-D-GLUCONATE 3-DEHYDROGENASE (EC 1.1
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PF00678; adh_short_C2;
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III.
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VII. VERY HYDROPHOBIC.
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EQAFDSIQT -> NKRLIPCKPSH (IN REF. 1).
MW; 889359C7 CRC32;
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KR1_HSVBS

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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE (EC 27, 1.-).
Bovine herpesvirus type 1.2 (strain ST).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
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BINDING
ACT_SITE
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"The complete DNA sequence and the genetic organization of the short
unique region (US) of the bovine herpesvirus type 1 (ST strain).";
Virology 199:409-421(1994).
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HSSP; P24941; 1AQ1.
401
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PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 94167875.
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164 462 PROTEIN KINASE.
170 178 ATP (BY SIMILARITY).
194 194 194 ATP (BY SIMILARITY).
279 279 BY SIMILARITY).
467 AA; 49885 MW; 25EBIE22 CRC32;
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MEDLINE; 98295987.

COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., COCLE S.T., BROSCH R., GAS S., BARRY C.E. III, TEKAIA F. BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R. BADCOCK K., BASHAM D., BROWN D., GENTLES S., HAMLIN N., HO DAVIES R., DEVLIN K., FEILWELL T., GENTLES S., HAMLIN N., HO DAVIES R., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J. RUTTER S., SEBGER K., SKELTON S., SQUARES S., SQARES R., SKILTON S., SULARES S., SCARES R., SKILTON S., SULARES S., SCARES R., SKILTON S., BARRELL B.G.; THE SEMONIA COMPLETE SOLUTION THE BEQUENCE.";

NATURE 393:537-544(1998).
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entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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JI-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 34, Last annotation update)
15-DEC-1996 (Rel. 34, Last annotation update)
15-DEC-1996 (Rel. 34, Last sequence)
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SUBCELUULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY A8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS PROTEIN SPECIFICALLY CATALYZES THE REMOVAL OF SIGNAL PEPTIDES FROM PROLIPOPROTEINS.

SIGNAL PEPTIDES FROM PROLIPOPROTEINS.

CATALYTIC ACTIVITY: CLEAVAGE OF "TERMINAL LEADER SEQUENCES FROM MEMBRANE PROLIPOPROTEINS. HUDROLYSES XAA-XBB-'|CYS, IN WHICH XAA IS HYDROPHOBIC (PREPERABLY LEU), XBB IS OFTEN SER OR ALA, XCC XAA IS HYDROPHOBIC (PREPERABLY LEU), XBB IS OFTEN SER OR ALA, XCC IS OFTEN GLY OR ALA, AND THE CYS IS ALKYLATED ON SULFUR WITH A
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S., SQARES R., SULSTON
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DOMAIN
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                                                                                                                                                                               EMBL; 274020; CAA98323.1; -
                                                                                                                                                                     PROSITE
KVVAVQLLPP
                  MPDEPTGSAD
                                   Length:
                                                                         109
1112
1112
1109
                                     202
GQPVSIIGDT
                  PLTSTEEAGG
                                                                          108
108
1111
132
132
180
                                    February 14,
                                                        21345
                                                                                                                                                  Hydrolase;
                                                   POTENTIAL.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
VTWTLVRNSG
                  AGEPNAPAPP
                                                                                                                                         se; Aspartyl protease; Transmembrane CYTOPLASMIC (POTENTIAL).
                                     2000
                                    08:02
AAFSMATGYT
                  RRLRMLLSVA VVVLTLDIVT
 WVLTLIATGV
                                     Þ
                                     Check:
                                      2319
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151 101

ADPSVVGGAI LLVILSIFGF

VVGIFWMGRR SVGWWPVFNV

LVSPWWALGL

GMILGGAMGN

LVDRFFRAPG

PLRGHVVDFI

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TRANSMEM 11
TRANSMEM 11
TRANSMEM 13
TRANSMEM 17
TRANSMEM 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHISTOSERDOV A.Y., BOYD J., MATHEWS F.S., LIDSTROM M.E.;
"A transcription-dependent DNase I-hypersensitive site in a far
upstream segment of the chicken alpha-globin gene domain coincides
with a matrix attachment region.";
Blochem. Blophys. Res. Commun. 184:1181-1189(1992).
-!- PATHMAY: METHYLAMINE UTILIZATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAN SPANNING R.J.M., DER PALEN C.J., SLOTI
STOUTHAMER A.H., DUINE J.A.;
"Expression of the mau genes involved in I
Paraccoccus denitrificans is under control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-OCT 1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
METHYLAMINE UTILIZATION PROTEIN MAUF.
                         MDH_RHILV
O33525;
                                                  SEQUENCE
                                                                                                    201
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                                                                                                                                                                                                                                                                                                                                                                     EMBL; U12464; AAA56723.1;
EMBL; M90099; AAA25579.1;
PIR; PH0856; PH0856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paracoccus denitrificans.
Bacteria; Proteobacteria;
 15-JUL-1998 (Rel. 15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 129-277 FROM N.A. MEDLINE; 92272712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcriptional activator.";
Eur. J. Biochem. 226:201-210(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAUF_PARDE P29897;
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                                                                           RHQENAALAD
                                                                                                    LLYMMTLAAV
                                                                                                                                                                               ASAAGPQPLW
                                                                                                                                                                                                                             Length: 277
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                                    STANDARD;
                                                                           GAILTALGAG
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                                                                                                                                                      YGLGALMLGG
                                                                                                                                                                               AVLGAAAVAG
                                                                                                                                                                                                       SAGQASVPDC
 36,
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79
131
152
199
225
277
                                                                                                                                                                                                                               February 14, 2000 08:02
                                                                                                                                                                                                                                                         28361 MW;
Created)
Last sequence update)
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                                                                              FTVLALI
                                                                                                                             DARQREPKWV
                                                                                                                                                      LLGGIGLIAG
                                                                                                                                                                               GLLSTWSPCG YSSISLLRPD
                                                                                                                                                                                                       KLFPQSPSAA TRIAVLLAAA LAGAAGGVAL
                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
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7BE517A2 CRC32;
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                                      PRT;
                                      320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277
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                                                                                                                             IGGLYGLSLG
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l of a LysR-type
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MDH_RHILV
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                                SEQUENCE FROM N.A.

STRAINERD / KW20;

MEDLINE; 95350630,

FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., MERRICK J.M.,

MCKENLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,

MCKENNEY K., SUTTON G., FITIZHUGH W., FIELDS C.A., GOCAYNE J.D.,

SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,

WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,

UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,

FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,

GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
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HSSP; Q27743; ILDG.
PROSTITE; PS00068; MDH; FALSE_NEG.
PFAM; PF00056; Idh; 1.
Oxidoreductase; Tricarboxylic acid cycle; NAD.
Oxidoreductase; Tricarboxylic acid cycle; NAD.
ACT_SITE 149 149
PROTON-RELAY (BY SIMILARITY).
SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
SCT_SITE 176 176
PROTON-RELAY (BY SIMILARITY).
SEQUENCE 320 AA; 33590 MW; 192E3E24 CRC32;
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01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

15-UUL-1999 (Rel. 38, Last annotation update)

PUTATIVE CELL CYCLE PROTEIN MESJ HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, MALATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                       MESJ OR
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Whole-genome random sequencing and
                                                                                                                                                                                                                                                                            laemophilus.
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                                                                                                                                                                                                                                                                                              us influenzae.
Proteobacteria;
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a; alpha subdivision; Rhizobiaceae group:
                                                                                                                                                                                                                                                                                              gamma
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                                                                                                                                                                                                                                                                                                subdivision;
assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            430
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MESJ_HAEIN Length: 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1.0
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                                     Myxococcus xanthus.";
J. Bacteriol. 175:4756-4763(1993).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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                                                                                use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             MEDLINE: 93328680.
MARTINEZ-CANAMERO M.,
                                                                                                                                                                                                                                                                                                                                               Myxococcales;
                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                     Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                  PUTATIVE LIPOPROTEIN MLPA PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenzae Rd.";
science 269:496-512(1995).
-i- SIMILARITY: BELONGS TO THE UPF0072 (MESJ/YCF62) FAMILY.
                                                  EMBL; S64103; AAB27615.1; -. PIR; B40609; B40609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                        PROSITE;
                                                                                                                                                                                                                                                 Oar, a 115-kilodalton membrane protein required for development of
                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
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0609; B40609.
; PS00013; PF
e; Signal; Li
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22
                                                                                                                                                                                                                                                                                                                                            Proteobacteria; delta les; Cystobacterineae;
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 ; Lipoprotein.
21 p
236 p
                                      PROKAR_LIPOPROTEIN; 1.
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                                                                                                                                                                                                                                                                             MUNOZ-DORADO J., FAREZ-VIDAL E., INOUYE M.,
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 POTENTIAL.
PUTATIVE LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                               Myxococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
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e; Myxococcus.
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 MLPA
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MML6\_MYCTU

Length: 397

February 14, 2000 08:02

101 151

AVKGTPMAGA GIYLAGTAAT

DPATPEGISH DLLIAGIAAL

VGTVALSLGA

51

MQGISVTGLV VALLPDEIAS

KRGWMVRSVF

DTIDGIDQLG

EQLASVIVIL

DKLAAIQPQL

QQINRELALA

NYATMSGIYA

LKLFLSADGK

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IIAA_SEQUENCE 1.0

IIAA_SEQUENCE 1.0

IIAA_MYCTU
AC Q10773;
AC Q10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TERAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD HORNSBY T., JAGELS K., KROCH A., MCLEAN J., MOULE S., MURRHY L., OLIVER S., OSBORNE J., QUALI M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J. TAYLOR K., HITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the SWISS Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@ibb-sib.ch).
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
PUTATIVE MEMBRANE PROTEIN MMPL6.
MMPL6 OR RV1557 OR MTCY48.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVGSGLNPEF AVVCQPTSAT GTTGYCVPAG DIPSFK
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                                                                                                                                                                                                                                                                 274020; CAA98334.1;
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236 AA;
                                       al protein; Transmembrane.
161 181 POTENTIAL.
190 210 POTENTIAL.
214 234 POTENTIAL.
214 234 POTENTIAL.
242 262 POTENTIAL.
293 313 POTENTIAL.
293 313 POTENTIAL.
330 350 POTENTIAL.
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24618 MW;
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              42421
                  MW;
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              9AFDFA0D
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                  CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration -
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GLVFAATMSS

VLALAVILLI AVGSDYNLLI ISRFKEEIGA GLNTGIIRAM AGTGGVVTAA

351

PRPASRMLRP FVFSDLRVLG

YGPRPVVREL

LLREGNDDPR

TQVATHR MTPSIAVLLG

QIGTTIGLGL LEDTLVVRAF

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RROCCOS DOT DACE
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                                       Ol-NOV-1995 (Rel. 32, Created)
Ol-NOV-1995 (Rel. 32, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
NEUROMEDIN B PRECURSOR.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L27235; -; NOT_ANNOTATED_CDS.
Oxidoreductase; NAD; One-carbon met
SEQUENCE 288 AA; 29736 MW; DEC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 176:1957-1968(1994).

-i- FUNCTION: MAY PLAY AN INTEGRAL ROLE IN METHYLOTROPHIC METABOLISM,

-i- CATALYTIC ACTIVITY: 5,10-METHYLENETETRAHYDROFOLATE + NAD(+) =

5,10-METHENYLTETRAHYDROFOLATE + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRALN=Ami / ....

MEDLINE; 94193542.

CHISTOSERDOVA L.V., LIDSTROM M.E.,

"Genetics of the serine cycle in Methylobacterium extorquens

"Genetics of the serine cycle in Methylobacterium extorquens

"Genetics of the serine cycle in Methylobacterium extorquens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
15-7UL-1999 (Rel. 38, Last annotation update)
METHYLENETETRAHYDROFOLATE DEHYDROGENASE [NAD+]
                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                         101
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Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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SEQUENCE FROM
                                                                                                                                                                           NEUB_XENLA
                             Kenopus.
                                                                                                                                                                                                                                                                                                                                                       51
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SIMILARITY: ONLY DISTANTLY RELATED TO THE OTHER 5,10-METHYLENE-THF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEHYDROGENASES.
                                                                                                                                                                                                                          GIGGLKLKLH
                                                                                                                                                                                                                                                                                         GRKLDKAQAA
                                                                                                                                                                                                                                                        LELLPQAAWQ
                                                                                                                                                                                                                                                                                                                                                         YTRGGKEKQS
                                                                                                                                                                                                                                                                                                                                                                                        MSKKLLFQFD
                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 288
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Z.A.
                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                            RACIAKLFES
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                                                                                                                                                                                                                                                                                                                         VKAAGGSVKG
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                                                                                                                                                                                                                                                         YNAQPPLGIG
                                                                                                                                                                                                                                                                                         NVTAAETADD ASRAEAVKGA
                                                                                                                                                                                                                                                                                                                         KKAVVLAGTG
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DEC1BD20 CRC32;
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                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                         SCMLDSNGSN
                                                                                                                                                                                                                                                           YGGKRAFGAL
                                                                                                                                                                                                                                                                                         HEVETAGAIG
                                                                                                                                                                                                                                                                                                                         AGEGAEVVLC
                                              Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                        Check:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration
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NEUB\_XENLA Length: 120

February

14,

2000

08:02

Type:

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Check: 1414

**A** 

14384

MW;

!!AA\_SEQUENCE 1.0

IFY\_KLEPN

STANDARD;

PRT;

229

B

101

DEIQWMLKKI MDDYIKTTQK GHFMGKKSLQ DTYNPSEQDM

51

μ

MSAVPLTRML

PLRFLTHLLL

DSEDFRPRII LSFIPLYFCM

EMIRGTFRQE PIRALSPRKQ EFSEDARNIE KIRRGNQWAI

01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence u. 01-FEB-1994 (Rel. 28, Last annotation

update)

CANNON F

SEQUENCE FROM N.A.
MEDLINE; 89041575.
BEYNON J., CANNON M.,

BANAN-WOLLASTON

۷.,

ALLY A.,

SUTTERQUIST nifW

nifY,

nifX and

genes of f

7

Klebsiella pneumoniae. Bacteria; Proteobacteria;

gamma subdivision; Enterobacteriaceae;

NIFY PROTEIN.

Klebsiella.

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ARNOLD W., RUMP A., KLIPP W., PRIEFER U.B., PUHLER A., "Nucleotide sequence of a 24,206-base-pair DNA fragment carrying entire nitrogen fixation gene cluster of Klebsiella pneumoniae.", Mol. Biol. 203:715-738(1988).

SIMILARITY: TO NIFX PROTEIN

ARNOLD

MEDLINE; 89094839.

Nucleic Acids Res.

16:9860-9860(1988).

"The nucleotide sequence of the nift, neumoniae.";

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PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl Acad. Sci. U.S.A. 89:9819-9822(1992).

1- FUNCTION: MAY BE A GROWTH FACTOR REQUIRED FOR THE HIGH RATE OF CELL DIVISION ENSUING AFTER FERTILIZATION, OR MAY HAVE A ROLE. SECRETAGOGUE THAT TRIGGERS THE RELEASE OF STORED COMPONENTS.

1- TISSUE SPECIFICITY: BRAIN, INTESTINE, AND OVARIES AND EARLY EMBRYOS (STAGES 2 AND 10).

1- SUMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BRAIN;
MEDLINE; 93028554.
WECHSELBERGER C., KREIL G., RICHTER K.;
WISCLAtion and sequence of a cDNA encoding bombosin like peptide from brain and early beautiful and control of the control of th
                                                                                                                                                                                                                                                 EMBL; L01530; AAA49912.1; - PROSITE; PS00257; BOMBESIN; Bombesin family; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY.
1
30
45
54
                                                                 Cleavage on
             NEUROMEDIN B.
AMIDATION (G-55 PROVIDE AMIDE GROUP)
F9870792 CRC32;
                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                 pair
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                                                                                                                                                                                                                                                      of basic residues;
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SO FFT SO
                                                                                 NIFY_KLEPN Length: 229
                                                          NOR1_ASPPA
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EMBL; X13303; CAA31670.1; -.
PIR; S01838; S01838.
Nitrogen fixation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  TRAIL F., CHANG P.-K., CARY J., LINZ J.E.;

"Structural and functional analysis of the nor-1 gene involved in the blosynthesis of aflatoxins by Aspergillus parasiticus.";

Appl. Environ. Microbiol. 60:4078-4085(1994).

-i. FUNCTION: MAY BE INVOLVED IN THE DEHYDRATION OF NORSOLORINIC ACII

-i. FORM AVERANTIN.

-i. PACHWAY: AFLATOXIN BIOSYNTHESIS.

-i. PACHWAY: AFLATOXIN BIOSYNTHESIS.

-i. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

FAMILY (SDR). STRONG, TO E.NIDULANS STCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
AFLATOXIN BIOSYNTHESIS KETOREDUCTASE NOR-1 (EC 1.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq.
15-DEC-1998 (Rel. 37, Last ann
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                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus parasiticus.
Eukaryota; Fungi; Ascomycot
Eurotiales; Trichocomaceae;
                                                                                                                                                     EMBL; L27801; AAA58798.1; PROSITE; PS00061; ADH_SHOI
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95085270.
TRAIL F., CHANG P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-ATCC 163 /
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                                                                                                 ACT_SIT
                                                                                                                            Oxidoreductase
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51
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                             MNGSLSQHDQ
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                                                      Length: 271
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                                                                                  28
185
271 AA;
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                                                                                                                                                        ADH_SHORT; FALSE_NEG.
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29569 MW;
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GLTGITLWKNAFFNPCFVLVAR
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HGVTHLDVVV ANAAMATNFG PASTMPLEHL QAHMMVNMYA PVLLFQATRI

"Sequence evolution in birds."; SEQUENCE FROM N.A. MEDLINE; 94141942. QUINN T.W., WILSON A.C.

and

around

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mitochondrial control

region

in

Mol. Evol. - CATALYTIC

37:417-425(1993) ACTIVITY: NADH +

UBIQUINONE

NAD(+)

Weognathae;

Metazoa; Chordata; Craniata; Vertebrata; Anseriformes; Anatidae; Anser.

Archosauria;

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THE REPORT OF THE PROPERTY OF 
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NUSM_ANSCE STANDARD; PRT; 214 AA.

031651;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
18-JUL-1998 (Rel. 36, Created)
18-JUL-1998 (Rel. 36, Last sequence update)
18-JUL-1998 (Rel. 36, Las
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15-JUL-1999 (Rel. 38, Last annotation update)
MINDI OR NDI OR NADH1.
COTURNIX TOTALLOR
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J. Mol. Evol. 32:153-161(1991)
CARRALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT I FAMILY.
SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT I FAMILY.

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Neognathae; Galliformes; Phasianidae; Phasianinae; (
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MEDLINE; 91178819.
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PROSITE; PS00668; COMPLEX1_ND1_2; PARTIAL.
PFAM, PF00146; NAD; Ubiquinone; Mitochondrion;
Oxidoreductase; NAD; Ubiquinone; Mitochondrion;
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                                                                                                                                                                                    NU6M_APILI Length: 167
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      EMBL; L06178; AAB96808.1; -.
Oxidoreductase; NAD; Ubiquin
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-THORAX;
MEDLINE; 93114603.
CROZIER R.H., CROZIER Y.C.;
The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization.";
Génetics 133:97-117(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P34857;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1.0
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                                                   151
                                                                                101
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Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoidea; Apidae; Apis.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apis mellifera ligustica (Common honeybee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
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                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
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                                                   LMTKITYIEK KTLRKKK
                                                                                  IIITMKIYNK LSQNEHYFNY
                                                                                                                                                   MMLTIIMLSK IFMSSLISMI
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                                                                                                                    ILMILIVELS
                                                                                                                                                                                      February 14,
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                                                                                                                                                                                                                      ; Ubiquinone; Mitochondrion.
19971 MW; 36B64E1B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGPEGLAELQ VAASKAATSM HTGLIKAYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SITAGMIITS FITPTKTPPM TMPLITKTAA
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                                                                                    FKNIDLMYLY
                                                                                                                      GMLIMFSYFI
                                                                                                                                                       LTIYLNNIFN
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                                                                                                                                                                                      2000
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                                                                                    MKMNSTLFFI MILMLIITLI
                                                                                                                    SLINEPLKLK MKPFIQTLFL
                                                                                                                                                                                      08:02 Type: P
                                                                                                                                                     SPSMLLIYLI
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STANDARD;

PRT;

263

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DEDTTO

NUM\_BRAOL STANDARD; PRT; 215 AA.

942027;

942027;

01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

NADH-UBIQUIONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (EC 1.6.5.3)

(EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD).

!!AA\_SEQUENCE 1.0

251

SEPYGPEVTR

DYFEDLTPET

IKQVLSALKE AIKEHLGIKO

SVTDVSKAPQ PGPQSGRQTC

ENAAGLTSLT

GETTPDGLFT YEVASFYTMY

101

CSISVMNEVA

RLLEMPPMRV

NRTPVGKFHV

QACTTTPCQL

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EXECUTIVE FROM N.A.

**X MEDILINE; 95034970.

**X MEDILINE; 95034970.

**X AZEVEDO J.E., DUARTE M., BELO J.A., WERNER S., VIDEIRA A.;

**X COMPLEX I from Neurospora.";

**X COMPLEX I SCHETRON ACCEPTOR FROM NADH TO THE RESPIRATORY

**X COMPLEX I SCHETRON ACCEPTOR FOR THE ENZYME IS BELIEVED

**X ENAMENT OF THE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED

**X COMPLEX I SCHEDNING OF THE FLAVOPROTEIN SUBJUINOL.

**X COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.

**X COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.

**X COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.

**X COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.

**X COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.

**X COMPLEX I INTER MEMBRANE.

**X COMPLEX I DATE OF THE STAVOPROTEIN FRACTION.

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                                                                                                     NUHM_NEUCR Length: 263 February 14, 2000 08:02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P40915;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE 24 KD SUBUNIT PRECURSOR (EC 1.6.5.3)
(EC 1.6.99.3).
                                                                                                                                                                                       METAL
METAL
METAL
METAL
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CHAIN
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Eukaryota; Fungi; Ascomycota; Euascomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X78083; CAA54990.1; -
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   51
                                                       ۳,
                                                       MATKLTPFLM RTAVRAATRL
      NTPDNNPDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                143
148
186
190
263 AA;
FKFSADNEKV
                                                                                                                                                                                          143
148
186
190
                                                                                                                                                               28842 MW;
   IEEIIKRYPP
                                                       STKPSTIAPV SRACLSISAR RPSDTLMVHR
                                                                                                                                                            MITOCHONDRION (POTENTIAL).

NADH-UBIQUINONE OXIDOREDUCTASE 24 KI
SUBUNIT.

IRON-SULFUR (2FE-2S) (POTENTIAL).

IRON-SULFUR (2FE-2S) (POTENTIAL).

IRON-SULFUR (2FE-2S) (POTENTIAL).

IRON-SULFUR (2FE-2S) (POTENTIAL).

IRON-SULFUR (2FE-2S) (POTENTIAL).
      QYKKAAVMPL
                                                                                                        Type: P Check: 3961
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      LDLGQRQHGF
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NUKM_BRAOL
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
SEQUENCE FROM N.A. STRAIN-K12 / ANS87; MEDLINE; 9389724. MEDLINE; 9389724. MEDIDNER U., GEIER S., PTOCK A., FRIEDRICH T., LEIF H., WEISS H.; "The gene locus of the proton-translocating NADH: ubiquinone oxidoreductase in Escherichia coli. Organization of the 14 genes relationship between the derived proteins and subunits of
                                                                                                                                                             P33605; P78236; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) NADH DEHYDROGBNASE I CHAIN J (EC 1.6.5.3) (NACHOREDUCTASE CHAIN 10) (NUO10).
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PROSITE; PS01150; COMPLEX1_20K; 1.
PFAM; PF01058; oxidored_q6; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Iron-sulfur; 4Fe-4S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-CV. SHOGUN
                                                                                                                                      Escherichia
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                                                                                                                         Proteobacteria;
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91
155
185
215
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A
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155
185
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215
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IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
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NADH-UBIQUINONE OXIDOREDUCTASE 20 KD
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                                                                                                                           subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Type:
                                                                                                                           Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transit peptide;
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(POTENTIAL).
(POTENTIAL).
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                  and
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!!AA\_SEQUENCE 1.0
ID NUZM\_NEUCR
AC P19968;
DT 01-FEB-1991 (\*

STANDARD;

A

151 101

EERAGEVLSN ILGVNDQGID

RKDDSAKRKT

GTPISAKAVG

AIMLVVIVYA **GLVVAFHVGR** 

P19968; 01-FEB-1991 (Rel.

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NUOJ_ECOLI Length: 184
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BLATTHER F.R., PITT
RILEY M., COT
GREGOR T.
                                                                                                          OXIGOREDUCTASE; N
TRANSMEM 1
TRANSMEM 28
TRANSMEM 54
TRANSMEM 92
TRANSMEM 138
CONFLICT 85
CONFLICT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORJUCHI T.,
IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
KASHIMOTO K., KINS., KIUNGA S., KITAGAWA M., KITAKAWA M., MAKINO K.,
MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
SUDMITCEG (JAN-1997) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: TRANSFER OF ELECTRON FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. DOSE COUPLE THE REDOX REACTION TO PROTON
TRANSLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F. GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                        TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsend an email to license@isbsib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12
                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                   ECOGENE;
                                                                                                                                                                                                                                                                                                                             EMBL; X68301; CAA48369.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                    BL; AE000317; AAC75540.1; -.
BL; D90859; CAB22037.1; -.
R; S37067; S37067.
R; S38319; S38319; S38319.
M; PF00499; Oxidored_q3; 1.
doreductase; NAD; Ubiquinone; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRADIENT.

CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNITS NUOA, H, J,

K, L, M, N CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SUBCELLULAR CONTROL OF THE NADH-UBIQUINOL OXIDOREDUCTASE
OF CHLOROPLASTS OR MITOCHONDRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
AGALEIIVYA
                              MEFAFYICGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex I.";
233:109-122(1993).
GAIMVLEVEV VMMLNLGGSE
                              IAILATLRVI
                                                           February 14, 2000
                                                                                            19874 MW;
                                THTNPVHALL
                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
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OPPB_ECOLI STANDARD; PRT; 305 cn.

p31132; p76026; p77550;

01-UUL-1993 (Rel. 26, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

01-NOV-1997 (Rel. 35, Last annotation update)

01-NOV-1997 (Rel. 35, ESTEM PERMEASE PROT
                                                                                                                                                                                                                                                                                MEDIINE; 9/426617...
MEDIINE; 9/426617...
BLATTWER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
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VIDEIRA A., TROPECHUG M., WERNER S.;

Primary structure, in vitro expression and import into mitochondria of a 29/21-kDa subunit of complex I from Neurospora crassa.";

Biochem. Biophys. Res. Commun. 166:280-285(1990).

1. FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON STROM ADH TO THE ENZYME IS BELIEVED TO BE UBIQUINONE.

70 BE UBIQUINONE.

1. CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

1. SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.

1. SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE. IMPORTATION INTO MITOCHONDRION IS MEMBRANE POTENTIAL DEPENDENT.
               IKEMOTO K.,
                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                       science
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15-DEC-1998 (Rel. 37, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE 21.3 KD SUBUNIT (EC 1.6.5.3)
(EC 1.6.99.3)
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Eukaryota; Fungi;
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                                                                                                                                                                                                                                  complete genome sequence of Escherichia coli K-12.";
nce 277:1453-1474(1997).
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     BABA T., FUJITA K., HAYASHI K., HONJO K., INADA T., ISONO K., ISONO S., ITOH
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Sordariaceae; Neurospora.
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HORIUCHI T.,
KANAI K., KASAI
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IIAA\_SEQUENCE 1.0

ID OPPB\_SALTY STANDARD;

AC P08005;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last seq

sequence

update) 306

PRT;

B

301

DPKIRY

ETIYGLPGIG

DYSLVLSLTI

LVGALTILEN

201

AKGLPMRRII QLFVNGALNR

LRHALKPALL PVLSYMGPAF VGIITGSMVI

VMIFAIILHW GAAAFFLAVI AKYHĻNDPIM

LPGGGWNGGA

LKFMILPMVA

LSLAYIASIA

101

LGVSAGVIAA TOYFSYLKOL

LKQNTKWDYT AHGDFGPSFK

VMGLAMTGVV IPSFVVAPLL

YKDYSVNDLV ASSFPVSAKI

51

MLKFILRRCL EAIPTLFILI Length: 306

February 14, 2000 08:02 Type: P Check:

5147

TISFFMMRLA PGSPFTGERT LPPEVMANIE

OPPB\_ECOLI

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DOMAIN
TRANSMEM
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SEQUENCE
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"Identification of the polyamine-induced protein as a periplasmic
oligopeptide binding protein."
J. Biol. Chem. 265:8387-8391(1990).
11. FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF
THE SUBSTRATE ACROSS THE MEMBRANE PROTEIN. INNER MEMBRANE.
11. SUBSTRATE ACROSS THE MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 ECOGENE; EG10675; OPPB
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
PFAM; PF00528; BPD_transp; 1.
Transport; Peptide transport; Transmembran
                                                                                                                                                                                                                                                              EMBL; AE000223; AAC74326.1; --
EMBL; D90763; CAB20709.1; --
EMBL; D90852; CAB21967.1; --
EMBL; J05433; -; NOT_ANNOTATED_CDS.
PIR; B36263; B36263.
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122
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306 AA;
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   MW.
CYTOPLASMIC (PROBABLE)
3FCCC9F5 CRC32;
                                      PROBABLE.
EXTRACELLULAR (PROBABLE)
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EXTRACELLULAR (PROBABLE)
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CYTOPLASMIC (PROBABLE).
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EXTRACELLULAR (PROBABLE)
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                                                                      CYTOPLASMIC (PROBABLE).
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TRANSLOCATION OF
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OPPB_SALTY
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PEARCE S.
                                                                                                                                                                                 TRANSMEM
DOMAIN
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Mol. Microbiol. 6:47-57(1992).
-i- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT
FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE
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Bacteria; Proteobacteria;
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OLIGOPEPTIDE TRANSPORT
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PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
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PIR; B29333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HILES I.D., GALLAGHER M.P., JAMIESON D.J., HIGGINS C.F.; Wolecular characterization of the oligopeptide permease salmonella typhimurium."; Mol. Biol. 195:125-142(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            topology of the integral membrane components, OppB and the oligopeptide permease of Salmonella typhimurium."; biol. 6:47-57(1992).
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 QLFVNGALNR DYSLVLSLTI LVGALTILEN AIVDVLYAVI
                       AKGLPMRRII FRHALKPALL PVLSYMGPAF
                                                                       IGVSAGVIAA
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                                                                                                                                                                                                                                                                                                                                transport;
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                                                                                                                                                                   33420
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T SYSTEM PERMEASE PROTEIN OPPB
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EXTRACELLULAR (PROBABLE).
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                                                                       VMGFAMTGVV
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MBL outstation -
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SEQUENCE FROM N.A.

MEDITINE; 91009258.

HUBER A., SMITH D.P., ZUKER C.S., PAULSEN R.;

"Opsin of Calliphora peripheral photoreceptors R1-6. Homology with Drosophila Rh1 and posttranslational processing.";

Drosophila Rh1 and posttranslational processing.";

J. Biol. Chem. 265:17906-17910(1990).

-I- FUNCTION: VISUAL PIGENITS ARE THE LIGHT-ABSORBING MOLECULES THE FUNCTION: VISUAL PIGENITS AND APOPROTEIN, OPSIN, COVALENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTL LINKED TO CIS-RETINAL.

-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-: PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES M BE PHOSPORYLATED:

-: MISCELLANEOUS: EACH EYE IS COMPOSED OF 800 FACETS OR OMMATIDIA.

-: MISCELLANEOUS: EACH EYE IS COMPOSED OF 800 FACETS OR OMMATIDIA.

-: PACH OMMATIDIUM CONTAINS, 8 PHOTORECEPTOR CELLS; RI-R8), THE R1

R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER CELLS.

-: MISCELLANEOUS: OPSIN RHI HAS AN ABSORPTION MAXIMA AT 480 NM.

-: SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ol-ANG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
01-DEC-1992 (Rel. 24, Last annotation update)
01-DEC-1992 (Rel. 24, Last annotation update)
0PSIN RH1 (OUTER R1-R6 PHOTORECEPTOR CELLS OPSIN).
0PSIN RH1 OR NINAE.
Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Calliphora, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                             DOMAIN
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GCRDB; GCR_(
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M58334;
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DOMAIN
                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                     hotoreceptor;
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  MW;
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CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
                                                                                                                                     5 (POTENTIAL)
CYTOPLASMIC.
                                                                                                                                                                                                        3 (POTENTIAL).
CYTOPLASMIC.
RETINAL CHROMOPHORE 6D98882F CRC32;
                                                      PROBABLE
                                                                     7 (POTENTIAL)
CYTOPLASMIC.
                                                                                                                                                                          4 (POTENTIAL)
EXTRACELLULAR
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CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                  .n; Transmembrane; Phed receptor; Vision. EXTRACELLULAR.
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                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371
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February

14,

2000

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Type:

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EMBL; K02315; AAA28733.1; AI
EMBL; K02320; AAA28735.1; AI
EMBL; K02316; AAA28735.1; JU
EMBL; K02317; AAA28735.1; JU
EMBL; K02318; AAA28735.1; JU
EMBL; K02319; AAA28735.1; JU
EMBL; K02319; AAA28735.1; JU
EMBL; K02319; AAA28735.1; JU
EMBL; AZ2012; OOFF
GCRDB; GCR_0028;
GCRDB; GCR_0029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
ZUKER C.
                                                                                                                                                                                          use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS-RETINAL.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
OPSIN RH1 (OUTER R1-R6 PHOTORECEPTOR CELLS OPSIN)
RH1 OR NINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZUKER C.S., COWMAN A.F., RUBIN G.M.;
"Isolation and structure of a rhodopsin gene from D. melanogaster.";
Cell 40:851-858(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'TOUSA J.E., BAEHR W.,
APPLEBURY M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 85176937.
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                                                                                                                                                                                                                                                                                                                    BE PHOSPHORYLATED.

MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR OMMATIDIA. EACH OMMATIDIUM CONTAINS 8 PHOTORECEPTOR CELLS (R1-R8), THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER CELLS.

CELLS.

MISCELLANEOUS: OPSIN RH1 HAS AN ABSORPTION MAXIMA AT 480 NM.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

OPSIN SUBFAMILY.
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1_DROME
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FBgn0002940; ninae.
PS00237; G_PROTEIN_RECEPTOR; 1.
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Coutstation -
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!!AA_SEQUENCE 1.0
ID OPS1_DROPS
AC P28678;
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RS STRAIN-APPLE HILL;

RX MEDILIE; 93012921.

RA CARULLI J.P., HARTL D.L.;

RE CONNECTION: VISUAL PICHENITS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OR A POPROTEIN, OPSIN, COVALENTLY

C. - INTECELLANEOUS: CRACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR DAWATIDIA. EACH OMMANIDIUM CONTAINS 8 PHOTORRECEPTOR CELLS (R1-R8),

C. - THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER

C. - INTECELLANEOUS: OPSIN RH1 HAS AN ABSORPTION MAXIMA AT 480 NM.

C. - INTECELLANEOUS: OPSIN RH1 HAS AN ABSORPTION MAXIMA AT 480 NM.
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DISULFID
BINDING
SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                           Drosophila pseudoobscura (Fruit fly).
Dukaryota: Metazoa; Arthropoda: Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Musc
Ephydroidea: Drosophilidae: Drosophila.
                                                                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
0PSIN RH1 (OTTER RI-R6 PHOTORECEPTOR CELLS OPSIN)
RH1 OR NINAE.
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DOMAIN
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EXTRACELLULAR.
5 (POTENTIAL)
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CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
CYTOPLASMIC.
PROBABLE.
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RETINAL CHROMOPHORE.
43B10BFA CRC32;
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CYTOPLASMIC.
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DISULFID
BINDING
SEQUENCE
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DOMAIN
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GCRDB; GCR_0429; -
GCRDB; GCR_0509; -
GCRDB; GCR_0509; -
FLYBASE; FBGn0012733; Dpse\ninaE,
FROSITE; PS00237; G_PROTEIN_RECEPTOR;
PROSITE; PS00238; OPSIN; 1.
PFAM; PF000001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X65877; CAA46708.1; -. PIR; S24605; S24605.
          SEQUENCE FROM N.A.
LIANG Z.Y., DEMARE
GLANSDORFF N.;
                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ORNITHINE CARBAMOYLTRANSFERASE, ANABOLIC (EC
                                                                                                                                                                        351
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Submitted (FEB-1997) to
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                                                   Vibrio sp. (strain 2693).
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                    DEMAREZ M.,
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n coupled
the
                     LEGRAIN C.,
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                                                   gamma subdivision; Vibrionaceae; Vibrio
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EMBL/GenBank/DDBJ
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RETINAL CHROMOPHORE.
AACD8CB5 CRC32;
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7 (POTENTIAL).
CYTOPLASMIC.
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EXTRACELLULAR.
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                     BAETENS M., ROOVERS
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                                                                                    2.1.3.3)
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                                                                                    (OTCASE).
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OTC_SCHPO
P31317;
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                                                                                                                                                                                            VAN HUFFEL C., DUBOIS E., MESSENGUY F.;
"Cloning and sequencing of arg3 and arg11 genes of
Schizosaccharomyces pombe on a 10-kb DNA fragment. Heterologous
expression and mitochondrial targeting of their translation
                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequ
15-JUL-1999 (Rel. 38, Last anno
ORNITHINE CARBAMOYLITRANSFERASE
(ORNITHINE TRANSCARBAMYLASE).
                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
-!- SUBCULULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00097; CARBAMOYLIRANSFERASE; 1.
PRAM; PF00185; OTCace; 1.
Arginine biosynthesis; Transferase.
SEQUENCE 301 AA; 32825 MW; 3CA3E90D CR
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                    -!- PATHWAY: FIRST STEP IN ARGININE BIOSYNTHESIS.
-!- SUBCELULAR LOCATION: MITCCHONDRIAL MATRIX.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                             STRAIN-972;
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                                                                      ORTHOPHOSPHATE
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                                                                                                                                                                      Biochem.
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copyright.
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annotation updat
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produced
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                                                                                                               WALSH S.V.;
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 collaboration
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SETTER DESCRIPTION OF THE CO.
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                                                                                                                               SEQUENCE FROM N.A.
SIQUENCE FROM N.A.
TISSUS-KIDNEY CORTEX;
MEDLINE; 97220379.
SIMONIC T., DUGA S., NEGRI A., TEDESCHI G., MALCOVATI M.,
TENCHINI M.L., RONCHI S.;
TENCHINI M.L., RONCHI S.;
TENCHINI M.L., RONCHI S.;
TENCHINI M.L., RONCHI S.;
TENCHINI M.J., 302:729-735(1997).
BIOCHEM. J. 322:729-735(1997).
-1- CATALYTIC ACTIVITY: D-ASPARTATE + H(2)0 + O(2) = OXALOACETATE +
NU''' Y 1 1/1/1/1/1
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                 NEUKL A., CECILIANI F., TEDESCHI G., SIMONIC T., RONCHI S.; "The primary structure of the flavoprotein D-aspartate oxidase beef kidney.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
D-ASPARTATE OXIDASE (EC 1.4.3.1) (DASOX) (D
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        J. Biol. Chem. 267:11865-11871(1992)
[2]
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NEGRI A., CECILIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
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EMBL; Z69727; CAA93560.1; -.
FIR; S2390; OWZP.
HSSP; Q51742; 1A15.
                                                             NH(3) + H(2)O(2).

-!- COFACTOR: FAD OR 6-HYDROXYFLAVIN ADENINE
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: PEROXISOMAL.
-!- SIMILARITY: BELONGS TO THE DAMOX/DASOX FA
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-338.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bovinae;
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(DASOX) (DDO)
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01-NOV-1997
15-DEC-1999
D-ASPARTATE
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BIOCHEM. 121:798-803(1997).

IBIOCHEM. 121:798-803(1997).

IBIOCHEM. 121:798-803(1997).

IBIOCHEM. 121:798-803(1997).

IBIOCHEM. 121:798-803(1997).

IBIOCHEM. 121:798-803(1997).

IBIOCHEM. INTERPRETATE OXIDATIVE DEAMINATION OF D-ASPARTATE.

ICATALYTIC ACTIVITY: D-ASPARTATE + H(2)O + O(2) = OXALOACETATE + H(3) + H(2)O(2).

INTERPRETATION: DEAMINATIVE DINUCLEOTIDE.

ICOPACTOR: PAD OR 6-HYDROXYFLAVIN ADENINE DINUCLEOTIDE.

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This SWISS-PROT entry is copyright. It is p between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
MEDLINE; 97306065.
SETOYAMA C., MIURA R.;
Structural and functional characterization of the human brain
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP; P00371; 1DAO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PROSITE; PS00342; MICROBODIES_CTER; 1.
PFAM; PF01266; DAO; 1.
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(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
OXIDASE (EC 1.4.3.1) (DASOX) (DDO)
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BY SIMILARITY.
BY SIMILARITY.

BY SIMILARITY OF THE SIGNAL (1)

MICROBODY TARGETING SIGNAL (1)

V -> I (IN SOME MOLECULES).

K -> R (IN REF. 1).

S -> G (IN REF. 1).

M; 842B960C CRC32;
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ght. It is produced through a collaboration Bioinformatics and the EMBL outstation. Bit in the are no restrictions on its titute. There are no restrictions on its ons as long as its content is in no way not removed. Usage by and for commercial eement (See http://www.isb-sib.ch/announce/
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Q15077; Q15754;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence updated)
T 15-DEC-1998 (Rel. 37, Last annotation upon P2Y purinoceptor 6 (P2Y6).
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 97432828.
MEDLINE; 97432828.
SOMERS G.R., HAMMET F., WOOLLA.
VENTER D.J.;
"Chromosomal localization of tl
phylogenetic analysis of the P3
Genomics 44:127-130(1997).
[3]
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HSSP; P00371
MIM; 124450;
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TISSUE-PLACENTA:
TISSUE-PLACENTA:
MEDILNE; 97415792
MAIER R., GLATZ A., MOSBACHER J., BILBE G.;
"Cloning of P276 cDNAs and identification of a pseudogene: cof P2Y receptor subtype expression in bone and brain tissues.
Biochem. Biophys. Res. Commun. 237:297-302(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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e EMBL/GenBank/DDBJ
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ISSING (IN ISOFORM DDO-2).
0948D6AB CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              human P2y6 purinoceptor gene purinoceptor family.";
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CONFLICT
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                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                   AF007892; AAB80713.1;
AF007891; AAB80712.1;
AF007891; AAB80712.1;
P34996; 1DDD.
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Length: 328
                                                                                                                                                                                                                                                                                     coupled
                             328
                             AA;
                                                                     February 14, 2000 08:02
                               36429
                               WW;
                                                                                                                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL)
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EXTRACELLULAR
                                          EXTRACELLULAR (
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3 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                               ISSING (IN REF. 29C125CE CRC32;
                                                                                                                                                     (POTENTIAL)
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         Check:
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PETP\_RHOCA P31078; 01-JUL-1993 (Rel. 01-JUL-1993 (Rel. 01-NOV-1995 (Rel. FYFTQKKFRR 1.0 STANDARD; RPHELLQKLT 326 Created)
Last sequence update)
Last annotation update) AKWOROGR 166 ₿

CYCLLACRIC

RODGPAEPVA QRNRTVCYDL SFORYLGICH ADLLYACSLP RENFKQLLLP

QERRGKAARM SPPALATHYM PLAPWHKRGG LLIYNYAQGD PVYSAVLAAG

AVVVAAAFAI

PTAIFAATGI HGSILFLTCI

AYLAVRSTPG

TAVYTLNLAL LGLPPTTCVY

LPLNICVITO

RRAAWLVCVA HWPFGDFACR

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MEDILINE; 92356828.

TOKITO M.K., DALDAL F.;

"petR, located upstream of the fbcFBC operon encoding the cytochrome bcl complex, is homologous to bacterial response regulators and necessary for photosynthetic and respiratory growth of khodobacter capsulatus.";
                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-MT1131;
                                                                                                                                                                                                                                                        Bacteria; Pı
Rhodobacter
                                                                                                                                                                                                                                                                              Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodoba
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II AA_SEQUENCE 1.0

IID PEX3_YEAST
AC PAB795;
DT 01-DEC-1992 (I
DT 01-DEC-1992 (I
DT 01-NOV-1997 (I)
DE PEROXISONAL MI
GN PEX3 OR PAS3 OR
OS SACCHATOMYCES
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RN [1]
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RX MEDLINE; 9137
RA HOEHFELD J.,
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C JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
A FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J.,
A KUCABA T., HALLSWORTH K., HANKINS J., HILLIER L., JIER M.,
A JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LET T.,
A JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LET T.,
A JOHNSON D., JOHNSTON L., LANGSTON W., HALLEY A., PEUUSO D.,
A RICKEN L., RILES L., TALCH A., TREVASKIE E., VIGNATI D.,
A RICKEN L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.,
A WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R.,
A RICKETTON: INVOLVED IN PEROXISOME BIOSYNTHESIS. MAY FUNCTION
C 1- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS THE
PEROXISOMAL-DEFICIENT PHENOTYPE AND MISLOCALIZATION IN THE
CYTOSOL OF PEROXISOMAL MATRIX PROTEIN. PEROXISOMAL.
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
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01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEROXISOMAL MEMBRANE PROTEIN PASS (PEROXIN-3).
PEXS OR PASS OR YDR329C OR D9798.15
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyceta; Fungi, Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
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MEDLINE; 91373453.
HOEHFELD J., VEENHUIS M., KUNAU W.-H.;
"PASJ, a Saccharomyces cerevisiae gene encoding a peroxisomal integral membrane protein essential for peroxisome biogenesis.";
J. Cell Biol. 114:1167-1178(1991).
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PIR: S22631; S22631
PROSITE; PS01117; HTH_MARR_FAMILY; 1.
PFAM; PF01047; Mark; 1.
Transcription regulation; DNA-binding.
SEQUENCE 166 AA; 18807 MW; 99E3E86E CRC32;
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PEX3_YEAST Length: 441 February 14, 2000
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EMBL; U32517; AAB64764.1; --
PIR; A40550; A40550;
SGD; L0001339; PAS3.
Transmembrane; Peroxisome.
DOMAIN
TRANSMEM
18
39
EMBL; J04987; AAA21973.1; -.
PIR; B34340; RDALAE.
HSSP; P19992; 2HSD.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_Short; 1.
PFAM; PF00678; adh_Short_C2; 1.
Oxidoreductase; NADP; PHB biosynthesis.
                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-416,
MEDLINE; 89359356.
MEDLINE; 89359356.
PEOPLES O.P., SINSKEY A.J.;
PEOPLES O.P., SINSKEY A.J.;
"Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes en Characterization of the genes encoding beta-ketothiolase acetoacetyl-CoA reductase.";
J. Biol. Chem. 264:15293-15297(1989).
-!- CATALYTIC ACTIVITY: (R)-3-HYDROXYACYL-COA + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p14697;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ACETOACETYL-COA REDUCTASE (EC 1.1.1.36).
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                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: SECOND STEP IN POLY-BETA-HYDROXYBUTYRATE BIOSYNTHESIS.
-!- SUBCELJULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE SHORT CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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441 AA;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL);
9C648B96 CRC32;
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MAGARARA COCCOCCOCCOCCETTTT AXCOCCUTTTTO

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PHBB_ALCEU Length: 246 February 14, 2000 08:02 Type: P
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EMBL; D90227; BAA14271.1; -.
EMBL; U144003; AAA95996.1; -.
EMBL; AE000482; AAC77058.1; -.
EMBL; J05260; AAA24349.1; -.
PIR; C35719; C35719.
ECOGENE; EG10720; PHNK.
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                   MEDLINE; 90170953.

CHEN C.-M., YE Q.-Z., ZHU Z., WANNER B.L., WALSH C.T.;

CHEN C.-M., YE Q.-Z., ZHU Z., WANNER B.L., WALSH C.T.;

CHEN C.-M., YE Q.-Z., ZHU Z., WANNER B.L., WALSH C.T.;

CHEN C.-M., YE Q.-Z., ZHU Z., WANNER B.L., WALSH C.T.;

Sequencing of the phn (psib) genes involved in alkylphosphonate sequencing of the phn (psib) genes involved in alkylphosphonate uptake and C.-P lyase activity in Escherichia coli B.",

J. BIOL. Chem. 265:4461-4471(1990)

J. BIOL. Chem. 265:4461-4471(1990)

FOR ALKYLPHOSPHONATES; PROBABLY RESPONSIBLE FOR ENERGY COUPLING FOR ALKYLPHOSPHONATES; PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE TRANSPORT SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1.0
PHNK_ECOLI
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                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructe you non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat)
PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                       "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes.", Nucleic acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 91193228.

MARKINO K., KIM S.K., SHINAGAWA H., AMEMURA M., NAKATA A.;

"Molecular analysis of the cryptic and functional phn operons phosphonate use in Escherichia coli K-12.";

J. Bacteriol. 173:2665-2672(1991).
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STRAIN=B;
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BURLAND V.D., PLUNKETT
BLATTNER F.R.;
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246 /
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Enterobacteriaceae;
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PROTEIN PHNK
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IIAA_SEQUENCE 1.0

IID 40708;

AC Q40708;

AC Q40708;

DT 01.NOV-1997 (Rel. 3)

DT 01.NOV-1997 (Rel. 3)

DT 01.NOV-1997 (Rel. 3)

DT 01.NOV-1997 (Rel. 3)

DE PIR7A PROTEIN.

OS OYZE SELVE (Rec.)

OS OYZE SELVE (REL. 3)

OR PIR7A PROTEIN.

RAN EIMMANN C., MAUCH RET STRAIN-CV. INDICA-I

RA REIMMANN C., MAUCH RET STRAIN (REL. 3)

CO -1- SIMILARITY: DIS COMMANN C. AND PART (REL. 3)

CC -1- SIMILARITY: DIS COMMANN C. AND PART (REL. 3)

CC -1- SIMILARITY: DIS COMMANN C. AND PART (REL. 3)

CC -1- SIMILARITY: DIS COMMANN C. AND PART (REL. 3)

CC -1- SIMILARITY: DIS COMMANN C. AND PART (REL. 3)

CC -1- SIMILARITY: DIS COMMANN C. AND PART (REL. 3)

CC -1- SIMILARITY: DIS COMMANN C. AND PART (REL. 3)

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CC SETTE SE
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    PI7A_ORYSA
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STRAIN-CV. INDICA-IR36;
STRAIN-CV. INDICA-IR36;
STRAIN-CV. INDICA-IR36;
STRAIN-CV. MAUCH F., DUDLER R., HOFMANN C.;
REIMMANN C., MAUCH F., DUDLER R., HOFMANN C.;
Physingae: requirement for the bacterial lema gene function.";
Physiol. Mol. Plant Pathol. 46:71-81(1995).
Physiol. Mol. Plant Pathol. 46:71-81(
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PFAM; PF00005; ABC_Tran; 1.

PFAM; PF00005; ABC_tran; 1.

PFAM; PF00005; ABC_tran; 1.

PFAM; PF00005; ABC_Transport; ATP-binding ALkylphosphonate uptake; Transport; ATP-binding ATP (BY SIMILARTY)

SEQUENCE 47 47 47 L-> O (IN REF. 2)

SEQUENCE 252 AA; 27831 MW; CBE59E63 CRC32;
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HSSP; P52704; 1YAS.
PFAM; PF00561; abhydrolase;
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Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                             Hydrolase; Serine esterase.
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Length: 263
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263 AA;
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AMERFPDKVA NTNQEPRTAV

HSLGGLSLAL FFMDSKTIVL

AAAGAHPARA

MEDGGKHFVF VHGLGYGAWC WYRVVAALRA AGHRAMALDM

01-MAY-1991 (Rel. 18, Creat 01-MAY-1991 (Rel. 18, Last 15-JUL-1998 (Rel. 36, Last PLASTOCYANIN PRECURSOR. PETE OR SLL0199.
Synechocystis sp. (strain Pacteria; Cyanobacteria; Ch

Last sequence up Created)

on update)

a PCC 6803). Chroococcales;

Synechocystis

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SEQUENCE
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EMBL; D64000; BAA11277.1; -.
PIR; S13733; S13733.
PDB; IPCS; I7-DEC-97.
PROSITE; P500196; COPPER BLUE; 1.
PFAM; PF00127; copper-bind; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The 2.15 A Crystal structure of a triple mutant plastocyanin from the cyanobacterium synechocystis sp. PCC 6803.";
J. MOI. B101. 275:327-336(1998).

-IP FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN P700 AND THE CYTOCHROME B/F COMPLEX IN PHOTOSYSTEM I.

-I- INDUCTION: BY COPPER.
                                                          METAL
METAL
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MEDLINE; 96127529.

TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,

KANEKO T., TANAKA A., SATO S.,

SUGIURA M., TABATA S.;

Sequence analysis of the genome of the unicellular cyanobacterium

Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb

region from map positions 64% to 92% of the genome.";

DNA Res. 2:153-166(1995).
                                                                                                                                      DOMAIN
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DE LA ROSA M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAZUKA T., OHARA O.;
"Towards a proteome project of cyanobacterium Synechocystis sp.
strain PCC6803: linking 130 protein spots with their respective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l)
SEQUENCE FROM N.A.
MEDLINE; 91338701.
MEDLINE; 91338701.
METHORS L.M., PECORARO V.L., MCINTOSH L.;
Copper-induced expression, cloning, and regulatory studies
"Copper-induced expression cloning, and regulatory studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 98128796
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MEDLINE: 97443974.
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SIMILARITY: CONTAINS ONE PLASTOCYANIN-LIKE DOMAIN.
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                              ; Copper;
28
126
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111
      WW,
                                                                                                                                                                                                          Signal; 3D-structure.
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PLEK\_HUMAN Length: 350

February 14, 40082 MW;

2000 08:02 Type:

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SEQUENCE

350 AA;

VARIANT

CA\_BIND DOMAIN DOMAIN

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312 101 347 92

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POTENTIAL

W -> R. /FTId=VAR\_005524. 04F9FC1F CRC32;

EMBL: X07743; CAA30564.1; -.
PIR: S00755; S00755.
PIR: A45762; A45762
PDB: 1PLS: 03-JUN-95.

PROSITE; PS50003; PH\_DOMAIN; PFADM; PF00169; PH; 2 PFAM; PF00610; DEP; 1.
PFAM; PF00610; DEP; 1.
Phosphorylation; Repeat; 3D-s
DOMAIN 107 120

N

3D-structure. CONTAINS 3 SITES.

POTENTIAL PHOSPHORYLATION

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"Solution structure of a pleckstrin-homology domain.";
Nature 369:672-675(1994).
-i- FUNCTION: MAJOR PROTEIN KINASE C SUBSTRATE OF PLATELETS,
EXACT FUNCTION IS NOT KNOWN.
-i- SIMILARITY: CONTAINS 2 PH DOMAINS.

MEDLINE; 94268557.
YOON H.S., HAJDUK P.J., PETROS A.M., OLEUNICZAK E.T.,

MEADOWS R.P.,

STI

J. Cell. Biochem. 40:133-145(1989)

R.A., HARLEY C.B.; the major protein

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STRUCTURE BY NMR OF 1-105.

FESIK S.W.;

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MEDLINE; 89359547.
TYERS M., HASLAM R.J., RACHUBINSKI
"Molecular analysis of pleckstrin:
substrate of platelets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYERS M., RACHUBINSKI R.A., SHORR R.G.L., HASLAM R.J., "Molecular cloning and exprosubstrate of platelets.", Nature 333:470-473(1988).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-AUG-1988 (Rel. 08, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation updat
PLECKSTRIN_(PLATELET P47 PROTEIN).
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I.J., HARLEY C.B.;
lexpression of the major protein kinase
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PLYA_MYCPO Length: 299
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Q12535;

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
PECTINESTERASE PRECURSOR (EC 3.1.1.11) (PECTIN
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Eukaryota; Fungi; Ascomycota; Euascomycetes; Loculoascomycetes;
Dothideales; Mycosphaerellaceae; Mycosphaerella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I5-DEC-1998 (Rel. 37, Created)
I5-DEC-1998 (Rel. 37, Last Sequence update)
I5-DEC-1998 (Rel. 37, Last annotation update)
PECTIN LYASE PRECURSOR (EC 4.2.2.10).
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STRAIN-DSM 62763 / BERKELEY BLOXOM;
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33072 MW;
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PECTIN LYASE.
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    METHYLESTERASE)
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PME_ASPAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHRISTGAÚ S., KOFOD L.V., HALKIER T., ANDERSEN L.N., H
DORREICH K., DALBOEGE H., KAUPPINEN S.;
"Pectin methyl esterase from Aspergillus aculeatus: ex
cloning in yeast and characterization of the recombina
Biochem. J. 319:705-712(1996).
Biochem. J. 319:705-712(1996).
IN MACEBATION AND SOFT-ROTTING
I- CATALYTIC ACTIVITY: PECTIN + N H(2)O - N METHANOL
I- SIMILARITY: BELONGS TO THE PECTINESTERASE FAMILY.
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Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                     _SEQUENCE 1.0
                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-7UL-1999 (Rel. 38, Last annotation update)
PECTINESTERASE PRECURSOR (EC 3.1.1.11) (PECTIN METHYLESTERASE)
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PROSITE; PS00503; PECTINESTERASE_2; 1.
PFAM; PFC1095; Pectinesterase; 1.
Hydrolase; Serine esterase; Cell wall; Signal.
SIGNAL 1 1 BY SIMILARITY.
CHAIN 18 331 PECTINESTERASE.
SEQUENCE 331 AA; 35681 MW; C567C2B3 CRC32;
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                                        "Nucleotide and derived amino acid sequence isolated from Aspergillus niger strain RH 53 Nucleic Acids Res. 18:4262-4262(1990).
                                                                                                                      STRAIN-RH
MEDLINE;
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspe
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                                                                                        KHANH N.Q., ALBRECHT JANY K.-D.;
                                                                                                                                                                                                             Aspergillus tubingensis.
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                                                                                                                                                  EQUENCE FROM N.A., AND
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                                                                                                          GOTTSCHALK M.,
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+ PECTATE:
                                                                                                                                                                                  Aspergillus
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                                                                             CDNA
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SEQUENCE FROM N.A MEDLINE; 92039066

\*\*RHANH N.Q., RUTTKOWSKI E., LEIDINGER K., ALBRECHT H., GOTTSCHALK M.;

\*\*Characterization and expression of a genomic pectin methyl esteraseencoding gene in Aspergillus niger.";

Gene 106:71-77(1991).

1- FUNCTION: INVOLVED IN MACERATION AND SOFT-ROTTING OF PLANT TISSUE.

1- CATALYTIC ACTIVITY: PECTIN + N H(2)O = N METHANOL + PECTATE.

1- CATALYTIC ACTIVITY: BECOMES TO THE PECTINESTERASE FAMILY.

1- CAUTION: STRAIN RH 5344 WAS PREVIOUSLY SAID TO BE FROM A.NIGER.

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IIAA_SEQUENCE 1.0

ID PSPB_BOVIN

AC P15781;

DT 01-ANG-1990 (R

DT 01-ANG-1990 (R

DT 01-ANG-1990 (R

DE (PULMONARY SURE

DE (PULMONARY SURE

CO ENARYYOLA; Met

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SEQUENCE OF 1-10.

MEDLINE; 88025136.

YU S.-H., CLHUNG W., OLAFSON R.W., HARDING P.G.R., POSSMAYER F.;

"Characterization of the small hydrophobic proteins associated pulmonary surfactant.";

Biochim. Biophys. Acta 921:437-448(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-ADR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-KUV-1997 (Rel. 35, Last annotation update)
01-KUV-1997 (Rel. 35, Last annotation update)
PULMONARY SURFACTANT-ASSOCIATED PROTEIN B (SP-B) (6 KD PROTEIN)
(PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)).
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                                                                                                                                                                                                  "Protein sequence analysis studies on the low molecular weight hydrophobic proteins associated with bovine pulmonary surfactant."; Biochem. Biophys. Res. Commun. 148:1406-1411(1987).
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EMBL: X54145: CAA38084.1; -.
PIR: X54445; CAA38084.1; -.
PIR: J70589. J70589.
PIR: J70589. J70589.
PROSITE: PS00503. PECTINESTERASE_1;
PROSITE: PS00503. PECTINESTERASE_2;
PRAM: PF01095: Pectinesterase: 1.
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331 AA;
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Length: 299

February 14, 2000 08:02 Type:

Check:

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151 101

HAVGNNMPKA AALAAVETVN

AGNPDILLVP TIEAGNILY PKMEATVNAA ALAQMYKRGÇ 51

GHQVEIVHAN

TPEESAKLAV AHAEDEEVIR

RAVHHKTADV

LMKGNVPTSV ARFLLTGDSK ש

VAVEDIPDED

MKLKDLIGKA KLNELTSSMQ

SIHKNKTIAV

AVKLAAEHLS

201

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IIAA_SEQUENCE 1.0

ID PTB_BACSU
AC P54530;
DT 01-OCT-1996 ()
DE PROBABLE PHOSI
E (PHOSPHOTRANS)
E PROSENTIANS
OS BACILLUS Subt
OC BACILLUS SUBT
OC BACILLUS SUBT
OC BACILLUS SUBT
OC TAKE
RL SUBMITTE ()
RA SATO T. TAKE
RL SUBMITTE ()
CC -1- SIMILARIT
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ALVEDLAR STABILITY BY LOWERING THE SURFACE TENSION AT THE AIR-
CC LIQUID INTERFACE IN THE PERIPHERAL AIR SPACES. SP-B INCREASES
THE COLLAPSE PRESSURE OF PALMITIC ACID TO NEARLY 70 MILLINEWTONS
CC -!- SUBGUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SUBGUNITHOMODIMER, DISULFIDE-LINKED.
CC -!- SUBGUNITHOMODIMER, DISULFIDE-LINKED.
CC -!- SUBGUNITHOMODIMER, DISULFIDE-LINKED.
CC -!- SUBGUNITHOMORATS SURFACTANT CONSISTS OF 90% LIPID AND 10%
PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
CC PROTEIN THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
CC CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
CC HYTTROPHOBIC PROTEINS (SP-B AND SP-C).
CRABOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
CC HYTTROPHOBIC PROTEINS (SP-B AND SP-C).
SP PIR; A29667; A29667.
PIR; M2967; Gaseous exchange.
SUFFACE Film; Gaseous exchange.
SEQUENCE 79 AA; 8660 MW; 2B73807E CRC32;
                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                             EMBL; D84432; BAA12594.1; -.
EMBL; Z99116; CAB14340.1; -.
SUBTILIST; BG11722; YGIS.
PFAM; PF01515; PTA_PTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOBAYASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S., SATO T., TAKEUCHI M.;
SUDMITTED (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYSES THE CONVERSION OF BUTYRYL-COA THROUGH
-PHOSPHATE TO BUTYRATE.
-!- CATALYTIC ACTIVITY: BUTANOYL-COA + ORTHOPHOSPHATE = COA +
BUTANOYLPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE PHOSPHATE ACETYLTRANSFERASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.

Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE PROSPHATE BOTYRYLTRANSFERASE (EC 2.3.1.19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-168 / JH642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE PHOSPHATE ACETYLTRANSFERASE AND
BUTYRYLTRANSFERASE FAMILY.
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299 AA; 3
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        1; Transferase; Acyltransferase
31772 MW; EF3F522D CRC32;
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251 SLIYFAKASV

AAVITGAKAP

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DESGMSQIDL

SLSKVVHKSF VEVNEEGTEA

AAATAAIMMM

RCARFVPRFC

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01-FEB-1994 (Rel. 28, Last
01-OCT-1996 (Rel. 34, Last
PLACENTAL THROMBIN INHIB:
(PROTEASE INHIBITOR 6).
PIG OR PII.
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P35237;
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1. SUBCELLULAR LOCATION: CYTOPLASMIC.
1. SIBST SPECIFICITY: HIGHEST LEVELS IN SKELETAL MUSCLE. ALSO FOUR TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL MUSCLE. ALSO FOUR PLACENTA, CARDIAC MUSCLE, LUNG, LIVER, KIDNEY AND PANCERAS.
1. SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94183847.
MORGENSTERN K.A., SI
CHING A., KISIEL W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94022386.

COUGHLIN P., SUN J., CERRUTI L., SALEM H.H., BIRD "Cloning and molecular characterization of a huma serine proteinase inhibitor.";

Proc. Natl. Acad. Sci. U.S.A. 90:9417-9421(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z22658; CAA80373.1;
EMBL; S69272; AAB30320.1;
PIR; S35750; S35750.
PIR; A48681.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      151
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PF00079; serpin; 1.

1; Serine profease inhibitor:

TTE 341 342 REACTJ

TCT 175 175 G -> 1

LTCT 362 362 R ->

LTCT 376 AA; 42587 MW; 2D8
EKFVEWTRLD
                                                                                                   SPGSVDPLTR
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MMDEEEVEVS LPRFKLEESY DMESVLRNLG MTDAFELGKA
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28, Last sequence update)
34, Last annotation update)
N_INHIBITOR (CYTOPLASMIC ANTIPROTEINASE) (CAP)
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                                                                                                      GNWDGQFDKE
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G -> E (IN REF. 2).
R -> S (IN REF. 2).
; 2D806418 CRC32;
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                                                                 PUR7_METTH 026272;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYTOPLASMIC ANTIPROTEINASE 2 (CAP2) (CAP-2) (PROTEASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351
15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PHOSPHORIBOSYLAMINOMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE
(SAICAR SYNTHETASE).
PURC OR MTH170.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                              351
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                        (EC 6.3.2.6)
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PUR7_METTH
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A ALDREDGE T., BASHIRADEH R., BLAKELY D., COOK R., GILBERT K.,
A HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
A SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
A JIWANI N., CARUSO A., BUSH D., SAFER H., PARWELL D., PRABHAKAR S.,
A MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
Complete genome sequence of Methanobacterium thermoautotrophicum
(T deltam: functional analysis and comparative genomics.")
L J. Bacteriol 179:7135-7155(1997)
C. -- CATALYTIC ACTUTTY: ATP + 1 - (5 - PHOSPHORIBOSYL) - 4 - CARBOXY - 5
- PHOSPHORIBOSYL) - 4 - (N - SUCCINO - CARBOXAMIDE) - 5 - AMINOIMIDAZOLE
C -- PATHWAY: SEVENTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
C -- SIMILARITY: BELONGS TO THE SAICAR SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                     PYRB.
Escherichia coli.
----ria; Proteobacteria;
                                                                                                                                                                                                                                           SEQUENCE 1.0
                              complementation.";
Proc. Natl. Acad. Sci.
                                                  SEQUENCE FROM N.A.
MEDLINE; 84119419.
SCHACHMAN H.K., PAUZA C.D., N.
"Location of amino acid alter
"Location of amino acid alter
transcarbamoylase: structural
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P00479; 047555;
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SEQUENCE FROM N.A. MEDLINE; 83195078.
                                                                                                                                                                 TRANSCARBAMYLASE)
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                                                                                                                                                                          1-JUL-1986 (Rel. 01, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
5-JUL-1999 (Rel. 38, Last annotation update)
SPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN
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E 248 AA;
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                                                                                                                                                                                                                       STANDARD; 047557;
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haeota; Methanobacteriales;
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28244 MW;
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                                 81:115-119(1984)
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QIU D.,
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                                                                           Y.R.;
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  REVISION TO 195.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
MEDLINE F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
GREGOR J., DAVIS N.W., KI
MAU B., SHAO Y.;
MAU B., SHAO Y.;
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STRAIN-K12 / MG1655;
MEDLINE; 95334362.
BURLAND V.D., PLUNKET;
BLATTNER F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Analysis of th
region from 92.
                                           STRAIN=K12 / W3110;
PASQUALI C., SANCHEZ
FRUTIGER S., PAQUET 1
HOCHSTRASSER D.F.;
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MEDLINE; 83169660.
TURNBOUGH C.L. JR.
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MEDLINE; 89017155.
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nce 277:1453-1474(1997).
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                               (SEP-1994)
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STRAIN-K12;
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MEDILINE, 83195079.

KONIGSBERG W.H., HENDERSON L.;

Amino acid sequence of the cattalytic subunit of aspartate transcarbanoylase from Escherichia coli.";

The sequence of the cattalytic subunit of aspartate transcarbanoylase from Escherichia coli.";

Natl. Acad. Sci. U.S.A. 80:2467-2471(1983).
SEQUENCE OF 1-20
STRAIN-K12 / EMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROLAND K.L., POWELL F.E., TURNBOUGH C.L. "Role of translation and attenuation in expression in Escherichia coli K-12."; J. Bacteriol. 163:991-999(1985).
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"Role of the ribosome in suppressing transcriptional the pyrBI attenuator of Escherichia coli K-12.";
Proc. Natl. Acad. Sci. U.S.A. 85:7149-7153(1988).
                    EMG2;
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                                                                                                                                                  SWISS-PROT
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APPEL R.D.,
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W MEDLINE; 91104728.

A GOUANUX J.E. STEVENS R.C., LIPSCOMB W.N.;

A GOUANUX J.E. STEVENS R.C., LIPSCOMB W.N.;

A GOUANUX J.E. STEVENS R.C., LIPSCOMB W.N.;

TCrystal structures of aspartate carbamoyltransferase ligated with representation and created by the constant ph.";

TC phosphonoacetamide, malonate, and CTP or ATP at 2.8-A resolution and representation ph.";

DECOMPANY CATELYTITY: CARBAMOYL-PHOSPHATE + ASPARTATE = CATALYTIC ACTIVITY: CARBAMOYL-SPARTATE - CATALYTIC PROBLEM RESOLUTION STEP IN PYRIMIDINE BIOSYNTHESIS.

C-!- SUBUNIT: HETERODOBCAMER (C23:3R2) OF SIX CREATALYTIC PYRE CHAINS ORGANIZED AS TWO TRIMERS (C3), AND SIX REGULATORY PYRE CHAINS ORGANIZED AS TWO TRIMERS (R2).

C--- SUBLILARITY: BELONGS TO THE ATCASSS/OTCASES FAMILY.
EMBL; K01472; AAA24476.1; --
EMBL; M10743; AAA2474.1; --
EMBL; M10743; AAA2474.1; --
EMBL; U14003; AAA97142.1; --
EMBL; M1003; AAA97142.1; --
EMBL; M60508; AAA24481.1; --
PIR; A00561; DTECC.
PDB; 1ACM: 15-JUL-92.
PDB; 1ACM: 15-JUL-92.
PDB; AATC; 15-CCT-90.
PDB; BATC; 31-JUL-94.
PDB; BATC; 31-JUL-94.
PDB; BATC; 31-JUL-94.
PDB; IRAA; 31-JAN-94.
PDB; IRAB; 31-JAN-94.
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SEQUENCE OF 1-5.

SETRAID-K12 / W3110;

MEDLINE; 98291876.

MOLLOY M.P., HERBERT B.R., WALSH B.J., TYLER M.I., TRAINI M.,

MOLLOY M.P., HERBERT B.R., WALSH B.J., TYLER M.I., TRAINI M.,

SANCHEZ J.-C., HOCHSTRANSER D.F., WILLIAMS K.L., GOOLEY A.A.;

"Extraction of membrane proteins by differential solubilization

separation using two-dimensional gel electrophoresis.";

selectrophoresis 19:837-844(1998).
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WEDLINE; 91104727.

STEVENS R. C., GOUAUX J.E., LIPSCOME W.N.;

STEVENS R. C., GOUAUX J.E., LIPSCOME W.N.;

"Structural consequences of effector binding to the T state of

"Structural consequences of effector binding to the T state of

aspartate carbamoyltransferase: crystal structures of the unligated
and ATP- and CTP-complexed enzymes at 2.6-A resolution.";

Biochemistry 29:7691-7701(1990).
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KE H.-M., HONZATKO R.B., LIPSCOMB W.N.;

Structure of unligated aspartate carbamoyltransferase coli at 2.6-A resolution.";

Proc. Natl. Acad. Sci. U.S.A. 81:4037-4040(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 97443975.
LINK A.J., ROBISON K., CHURCH G.M.;
"Comparing the predicted and observed
in the genome of Escherichia coli K-12
Electrophoresis 18:1259-1313(1997).
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ECOGENE; EG10805; PYRB.
PROSITE; PS00097; CARBAMOYLIRANSFERASE;
PFAM; PF00185; OTCace; 1.
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ECO2DBASE; H031.3; 6TI
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HELIX SEQUENCE

285 310 AA;

304 34296 MW;

BDF9E927 CRC32;

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I!AA_SEQUENCE 1.0

ID PYRB_MXCTU

AC P71808;

CO 1-NOV-1997 (F

DT 01-NOV-1997 (F

DT 01-NOV-1999 (F

DE TRAIN-HATTE SAME

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RA COLE S.T., BR

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                 PYRB_MYCTU
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GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKALA F.,
BANCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HALLIN N., HOL-
HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURRHY
OLLVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.
RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULS
TAYLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from t
complete genome sequence.";
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content entitles and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend.an.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence.";
Nature 393:537-544(1998).
-!- CATALTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE
ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE.
-!- PATHWAY: SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                       EMBL; Z81011; CAB02641.1; -.
HSSP: P00479; 3AT1.
PROSITE: PS00097: CARBAMOYLTRANSFERASE;
PFAM; PF00185; OTCace; 1.
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PYRB OR RV1380 OR MTCY02B12.14.

Mycobacterium tuberculosis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Corynebacteriheae; Mycobacteriaceae; Mycobacterium.
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01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1
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          Length: 319
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                                                      biosynthesis; Transferase.
319 AA; 33818 MW; 38CF9A86 CRC32;
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2.1.3.2) (ASPARTATE
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Type: P Check: 1547
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tions on its
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101

MTPRHLLTAA FYENSTRTRV ADALIIRHPA

SGAAHLLAQW TGAHNDGPAV INAGDGTHEH PTQALLDALT

SSVGKGESLR DTALTLRAAG

PRT, 308 AA.

D PYRB\_PYRHO STANDARD; PRT; 308 AA.

AC 058451;

DT 15-DEC-1999 (Rel. 39, Careated)

DT 15-DEC-1999 (Rel. 39, Last sequence update)

DT 15-DEC-1999 (Rel. 39, Last annotation update)

DT 15-DEC-1999 (Rel. 39, Last annotation update)

ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) (ASPARTATE

101 151 201 251 301

NLKVLEKAKD LALVLGVI

ELRIMHPLPR VDEIHPEVDN TKHAIYFRQV

PYRB\_PYRAB

Length: 308

February 14, 2000 08:02 Type: P Check:

9304

51

MDWKGRDVIS IRDESKEDIE TVLATAERLE RELKEKGQLE YAKGKILATU FFEDSTRTRL SFESAMHRLG GAVIGFAEAS TSSVKKGESL RDTIKTVEQY

CDVIVIRHPK

EGAARLAAEV

GRIDGLKIGL ELREKGMKVV

LGDLKYGRTV

AEVPVINAGD HSLAEALTFY KLDVLYVTRI

GSNQHPTQTL DVELYLISPE QKERFPDEQE

LDLYTIKKEF

51

SFEVAGKWMS

DLSRDDATAI LDDADRFAQA LVGRDIKKLP TLRGRTVVTM

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!!AA_SEQUENCE 1.0
EMBL; U61765; AAB62984.1; -.
HSSP; P00479; 3AT1.
PROSITE; P500097; CARBAMOYLTRANSFERAS
PFAM; PF00185; OTCACe; 1.
Pyrimidine biosynthesis; Transferase.
SEQUENCE 308 AA; 34901 MW; 7CEC71
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial contents are requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-7UL-1999 (Rel. 38, Last annotation update)
ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) (ASPARTATE TRANSCARBAMYLASE) (ATCASE).
                                                                                                                                                                                                                                                                                                                                                             Pyrococcus abyssi
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                                                                                                                                                                                                                                                                                                                                                  Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                    CARBAMOYLTRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                              Thermococcales; Thermococcaceae; Pyrococcus.
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 7CEC7D77 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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01-AUG-1988 (Rel. 08, Created)
01-BUG-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARTATE CARBAMOYLIRANSFERASE CATALYTIC CHAI
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PROSTITE; PS00097; CARBAMOYLTRANSFERASE; 1.
PFAM; PF00185; OTCace; 1.
Pyriniddine biosynthesis; Transferase.
SEQUENCE 308 AA; 34862 MW; 12633B0D CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence and gene organization of the genome of a thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).

-i- CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE = ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE.

-i- PATHMAY: SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.

-i- SUBUNIT: CONTAINS CATALYTIC AND REGULATORY CHAINS.

-i- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMIYA M., OHUKU Y.,
SAKAI M., OGURA K., OTSUKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI
FUNNHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI
ANYU K. NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1.0
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Archaea; Euryarchaeota;
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PYRB OR PH0720.
MEDILINE; 87246692.

MEDILINE; 87246692.

MICHAELS G., KELLN R.A., NARGANG F
"Cloning, nucleotide sequence and
Salmonella typhimurium LT2.";
Eur. J. Biochem. 166:55-61(1987).
                                                                                                                                                                                                                                                                Salmonella typhimurium
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                                                                                                       STRAIN-LT2
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                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        Proteobacteria;
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2 MW; 12633B0D CRC32;
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                                                          of.
                                                                                                                                                                                                                                        Enterobacteriaceae
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                                                   pyrBI
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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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PIR; S00049; OWEBAC.
HSSP; P00479; 1RAG.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                 01-FEE-1991 (Rel. 17, Created)
01-FEE-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN
TRANSCARBAMYLASE) (ATCASE).
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STYGENE; SG10324; PYRB.
PROSITE; PS00097; CARBAMOYLTRANSFERASE;
PFAM; PF00185; OTCace; 1.
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NIT_MET 0 0 BY SIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE ORTHOPHOSPHATE + N-CARBAMOYL-ASPARTATE.
PATHWAY: SECOND STEP IN PREIMIDINE BIOSYNTHESIS.
SUBUNIT: HETERODODECAMER (2C3:3R2) OF SIX CATALYTIC ORGANIZED AS TWO TRIMERS (C3), AND SIX REGULATORY PY ORGANIZED AS THEE DIMERS (R2).
SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                     SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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                                                                                                                                                                                                                                                   Proteobacteria;
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                                                                                                                                                                                                                                                 gamma subdivision;
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PYRB_VIBS2
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PYRB_VIBS2
P96174;
                             EMBL; Y09786; CAA70923.1; -.
HSSP; P00479; IRAG.; CARBAMOYLIRANSFERASE; 1.
PROSITE; PS00097; CARBAMOYLIRANSFERASE; 1.
PFAM; PF00185; OTCace; 1.
PYINITATION blosynthesis; Transferase.
SEQUENCE 310 AA; 34419 MW; C460D24E CR
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pyrimidine biosynthesis; Transferase.

INIT_MET 0 0 BY SIMII

SEQUENCE 305 AA; 33240 May.
                                                                                                                                                                                                                                                         SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio sp. (strain 2693).
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN
TRANSCARBAMYLASE) (ATCASE).
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   Length: 310
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P00479; 1RAG.
TE; PS00097; CAI
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 February 14, 2000 08:02
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                                 C460D24E CRC32;
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Type: P Check:
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DAFVMRHPQE GAARLASEFS NVPVINGGDG

SNQHPTQTLL

DLFSIYETQG

!!AA\_SEQUENCE 1.0 ID RA51\_DROME AC Q27297;

STANDARD;

PRT;

336

3

151 201 251

AQEVAL

LKQEYAHKEV

YLSMEERMGC

GIGACFACVC

HINESETSYV KVCLDGPVFF

YVATADGSYG

ETGEVTDVIK

RKKLEFDILL

EASTRIRLSF ETAIQRLGGT VIGFDNASNT SLAKKGETLA DSISVISSYV

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LELIVKTAAK LKKQPQPELL

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PYRZ_BACSU Length:
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ID PYRZ_BACSU
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KAHLER A.E., SWITZER R.L.;

RAHLER A.E., SWITZER R.L.;

REQUISED SUBSTITUTE OF A CONTROL OF 
   101
                                                                                                                                                                                                                         EMBL; M59757; AAA21271.1; -.
EMBL; Z99112; CAB13427.1; -.
PIR; G39845; G39845; G39845; SUBTILIST; BG10717; PYRDII.
Pyrimidine biosynthesis; Electron transport.
Pyrimidine biosynthesis; S164D3B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; Bacillus/Clostridium group.
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OUINN C.L., STEPHENSON B.T., SWITZER R.L.; "Functional organization and nucleotide se subtilis systandine biosynthetic operon."; J. Biol. Chem. 266:9113-9127(1991).
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01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
DIHYDROOROTATE DEHYDROGENASE ELECTRON TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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      VNEVQPGKTA LLVGGGVGVP
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DEHYDROGENASE ELECTRON TRANSFER SUBUNIT.
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                                                               FEKNEVTIIY
                                                                                                                     NQQIADRVFQ
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                                                                                                                                                                          February 14, 2000 08:02 Type:
                                                        RVDGEGTRLL
                                                                                                                 MVLKGELVQG FTTPGQFLHL KVSEAVTPLL
   PLQELSKRLI
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EKGVNVIHVL
                                                        SLKQQGELVD
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   GFQSAKDVF
                                                            VLGPLGNGFP
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IIAA_SEQUENCE 1.0

ID RBCK_CHRVI STANDARD; PRI;
AC P25544;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence)
DT 01-MAY-1992 (Rel. 22, Last annota)
THAY-1992 (Rel. 22, Last annota)
THAY-1992 (Rel. 22, Last annota)
                                                                                                                                                                                                                                                                                                                               OSCHOOL
                                                                                                                                                                                                                                                                                                      RA51_DROME Length: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CANTON-S;
MEDLINE; 93161094.
AKABOSHI E., INOUE Y., RYO H.;
"Cloning of the cDNA and genomic DNA gene of Drosophila melanogaster.";
Jpn. J. Genet. 69:663-670(1994).
[2]
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01-NOV-1997 (Rel. 35
15-DEC-1999 (Rel. 35
DNA REPAIR PROTEIN F
                                                                                                                                                                                                                                                                                                                                           FLYBASE; FBgn
DNA-binding;
NP_BIND 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITINE; 96207535.

MCKEE B.D., REN X.J., HONG C.S.;

"A recA-like gene in Drosophila melanogaster that is e
high levels in female but not male meiotic tissues.";
Chromosoma 104:479-488(1996).
-i- FUNCTION: BINDS TO SINGLE AND DOUBLE STRANDED DNA
DNA-DEPENDENT ATPASE ACTIVITY. UNDERWINDS DUPLEX I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                               EMBL; D37788; BAA07039.1; -. EMBL; D17726; BAA04580.1; -. EMBL; L41342; AAA64873.1; -.
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 Chromatium vinosum
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336 AA;
                                                                                                                                                                                                                                                                                                                               ATP-binding; Nuclear protein.
124 131 ATP (POTENTIAL).
36 AA; 36647 MW; 5BD6F6D2 CRC32;
                                                                                                                            YDSPCLPESE
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35, Last sequence update)
39, Last annotation update)
N RAD51 HOMOLOG (RECA PROTEIN
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UKARYOTIC RECA-LIKE PROTEIN; SOME,
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Transcription regulation: Activator: DNA-binding.
DNA\_BIND 20 39 H-T-H MOTIF (BY SIMILARITY).
SEQUENCE 302 AA; 34092 MW; CA38CF20 CRC32;

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Bacteria; Protection Allochromatium.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-57 FROM N.A.

MEDLINE; 89213919.

VIALE A.M., KOBANSHI H., AKAZAWA T.;

"Expressed genes for plant-type ribulose 1,5-bisphosphate

"Expressed genes for plant-type ribulose 1,5-bisphosphate

carboxylase/oxygenase in the photosynthetic bacterium Chromatium

vinosum, which possesses two complete sets of the genes.";

Bacteriol. 171:2391-2400(1999).

"Bacteriol. 171:2391-2400(1999).

"Bacteriol. TRANSCRIPTIONAL REGULATOR OF RUBISCO

GENES (RECAB) EXPRESSION.

"SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL

"REGULATORS.
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIALE A.M. KOBAYASHI H., AKAZAWA T., HENIKOFE S.;
"rbcR, a gene coding for a member of the LysR family of
transcriptional regulators, is located upstream of the er
of ribulose 1,5-bisphosphate carboxylase/oxygenase genes
photosynthetic bacterium Chromatium vinosum.";
paacteriol. 173:5224-5229(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 91317745.
VIALE A.M., KOBAYASHI
                                                        EMBL; M64032; AAA23327.1; --
EMBL; M26396; -; NOT_ANNOTATED_CDS.
PIR; A40369; A40369.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
PFAM; PF00126; HTH_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria;
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RBCR\_CHRVI Length: 302 P10647;
01-7UI-1989 (Rel. 11, Created)
01-7UI-1989 (Rel. 11, Last sequence update)
01-7UI-1989 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN
(EC 4.11.39) (RUBISCO SMALL SUBUNIT C). RBS0\_SOLI 301 251 201 151 101 core eudicots; Solanum tuberosum (Potato) Eukaryota; Viridiplantae; 51 Ь SOLTU r F ETRRLVTLDV TROAMERFFS PRNVEVEAEA STVNYFAPRL ERLGKQVVLT MHVSLRQLRV FEAVARHNSY TRAAEELHLS QPAVSMQVRQ sum (Potato).
idiplantae; Streptophyta; Embryophyta; Tracheophyta;
idiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Spermatophyta; Magnoliophyta; eudicotyledons;
Steridae; euasterids I; Solanales; Solanaceae; STANDARD; EGFPDRRQWY ERGOTIRHGM **FMDNPLVVIA** MAIFQQRHSG EAGREVFHYS February 14, LVYRRGKRLS QMTRNEAVKQ PPDHPLAGER IGLRLDVINR RAIGQSLREM PRT; 2000 08:02 181 ESLVQMLDSN EEVLESLKGV PAAGAFREFV AVRSGLGLSV AISLARLAEE ₿ Type: 0 VSLHTIELEL SVDLVLMGVP LEDEIGLSLF LSEAARMHCR SRGSLRIAVA Þ Check: 4295

SEQUENCE Solanum.

FROM

N.A.

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NAME TO COLOR OF THE PROPERTY AND COLOR OF T
RBS0_SOLTU Length: 181 February 14, 2000 08:02
                                                                             SEQUENCE FROM N.A. STRAIN=CV. VF36; MEDLINE; 87163513. MCKNIGHT T.D., ALEX.
                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 P
(EC 4.1.1.39) (RUBISCO SMALL SUBUNIT 1) (LESS17).
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MEDLINE; 88124937.

WOLTER F.P., FRITZ C.C., WILLMITZER L., SCHELL J., SCHREIER P.H.;

"TDCS genes in Solanum tuberosum: conservation of transit peptide and

"rDCS genes in Solanum tuberosum: conservation of transit peptide and

"rDCS genes in Solanum tuberosum: conservation of transit peptide and

"ROS genes in Solanum tuberosum: conservation of transit Acad. Sci. U.S. A. 85:846-850(1988).

PROCESSION RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF

"TO-RIBULOSE 1.5-BISSHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNVHETIC

CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAMENIVATION OF

THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH

REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME

ACTIVE STEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _SEQUENCE 1.0
RBS1_LYCES
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MENDEL; 15074; SOLTU;rbcS;mn15074.

PFAM; PF00101; RuBisCO_small; 1.

Photosynthesis; Carbon dioxide fixation; Photorespiration; Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit
                      MCKNIGHT T.D., ALEXANDER D.C., BABCOCK M.S., SIMPSON R.I "Nucleotide sequence and molecular evolution of two tome encoding the small subunit of ribulose-1,5-bisphosphate
                                                                                                                                                                                                                    Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
Solanum.
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TRANSIT
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181
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RIBULOSE BISPHOSPHATE CARBO
CHAIN C.
; 44574D48 CRC32;
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                                                         tomato
                                                                                   R.B.;
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EFETERGFVY RENNSSPGYY

DGRYWTMWKL PMFGCTDATQ VLAEVQEAKK

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SMVAPFTGLK SAASFPVTKK

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MASSIVSSAA AATRSNVAQA

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STETE SERVICE 
            RBS1_LYCES
                                                                                                        CONFLICT
SEQUENCE
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-i- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PRIMOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE STREET
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MEDLINE; 88038372.
SUGITA M., MANZARA T., PICHERSKY E., CASHMORE A., GRUISSEM W.;
"Genomic organization, sequence analysis and expression of all
genes encoding the small subunit of ribulose-1,5-bisphosphate
carboxylase/oxygenase from tomato.";
Mellone 1000-21-25(1087),
Mellone 2000-21-25(1087),
Mel
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M15235; AAA34191.1; -. EMBL; M13542; AAA34188.1; -. EMBL; X05982; CAA24400.1; -. EMBL; X66068; CAA46868.1; -. EMBL; X66068; CAA46868; CAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-20 FROM N.A. (RECS-1)
STRAIN-CV. VENT CHERRY LA1221; TISSUE-ROOT;
MEDIJINE: 93144693
MANZARA T., CARRASCO P., GRUISSEM W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PICHERSKY E., BERNATZKY R., TANKSLEY S.D., CASHMORE A.R.; "Evidence for selection as a mechanism in the concerted ev Lycopersicon esculentum (tomato) genes encoding the small ribulose-1,5-bisphosphate carboxylase/oxygenase."; Proc. Natl. Acad. Sci. U.S.A. 83:3880-3884(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Gen. Genet.
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                                                                                                                                                                                                                                                                                                                                                                                      P00866; 1RIC.

P000101; RubisCO_small; 1.

PF00101; RubisCO_small; 1.

Synthesis; Carbon dioxide fixation; Photorespiration;

Synthesis; Carbon dioxide fixation; Photorespiration;
            Length: 181
                                                                                                                                                                                                                                                                                                                                                                                family.
                                                                                                              181 AA;
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                                                                                                                                                                                                                                                                        58
181
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RRY LA1221;
                                                                                                              79 I
20307 MW;
      February 14, 2000
                                                                                                                                                         CHLOROPLAST (BY SIMILARITY)
RIBULOSE BISPHOSPHATE CARBO
CHAIN 1.
L -> E (IN REF. 1).
                                                                                                              -> F (IN REF. 1).
981E9B5C CRC32;
            08:02
טי
                                                                                                                                                                                                                                                                              CARBOXYLASE SMALL
            Check:
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11 subunit
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OF THE SERVICE OF THE
!!AA_SEQUENCE 1.0 ST.
ID RBS1_SOLTU ST.
AC P26574;
DT 01-AUG-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                             RBS1_PETSP Length: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_SEQUENCE 1.0
RBS1_PETSP
P04714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
TUMER N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions with the property institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carboxylase are expressed differentially in petunia leaves.";

Nucleic Acids Res. 14:3325-3342(1986).

-!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF

D-RIBULOSE 1,5-BISCHOSPHATE, THE PRIMARY EVENT IN PROTOSYNTHETIC

CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF

THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION FRACESS. BOTH

REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petunia sp. (Petunia).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Sólanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN
(EC 4.1.1.39) (RUBISCO SMALL SUBUNIT SSU8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X03820; CAA27444.1; -. PIR; A24917; RKPJS8. HSSP; P00866; IRLC.
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit
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                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MENDEL; 15078; PETSp;rbcS;mn15078.
PFAM; PF00101; RuBisCO_small; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyase; Oxidoreduc
Multigene family
TRANSIT
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3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: CHLOROPLAST.
SINILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVE SITE.

CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE +
2 3-PHOSPHO-D-GLYCERATE.
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                                                       STANDARD;
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                                                                                                                                                                                                                                                                                         VATRINVAQA
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   23, Created)
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                                                                                                                                SFIAYKPPGF
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RIBULOSE BISSHOSPHATE CARBOXYLASE SMALL
CHAIN SCUB.
, 71E5C2F3 CRC32;
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RBS1_SOLTU
                                               : AA
RBS2_LYCES
P07179;
01-APR-1988 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-CV. AM 80.5793;

FRITZ C.C., WOLTER F.P., SCHENKEMEYER V., HERGET T., SCHREIER P.H.;

FRITZ C.C., WOLTER F.P., SCHENKEMEYER V., HERGET T., SCHREIER P.H.;

SUBMILTED (DEC-1992) to the EMBL/GenBank/DDBJ databases.

SUBMILTED (DEC-1992) to the EMBL/GenBank/DDBJ databases.

FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE TIXATION, AS WELL AS THE OXIDATIVE FRACMEMTATION THE PRIMARY EVENT IN THE PHOTORESPIRATION PROCESS. BOTH THE PRIMARY CONTRACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME

REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR
(EC 4.1.1.39) (RUBISCO SMALL SUBUNIT 1).
RBCS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 88124937.

WOLTER F.P., FRITZ C.C., WILLMITZER L., SCHELL (
"rbcS genes in Solanum tuberosum; conservation (
exon shuffling during evolution.";
exon shuffling during evolution. 85:846-850(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                            101
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                    Lyase; Oxi
Multigene
                                                                                                                                                                                                                                                                                                                 PIR; B31083; RKPOSI.

PIR; S31497; S31497.

HSSP; P00866; IRLC.

MENDEL; 490; SOLtu;rbcS;l.

MENDEL; 490; SOLtu;rbcS;l.

PFAM; PF00101; RuBisCO_small; l.

PFAM; PF00101; RuBisCO_small; l.

Photosynthesis; Carbon dioxide fixation; Photorespiration;

Photosynthesis; Carbon dioxide fixation; Chloroplast; Transit

Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-HH1201/7;
                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X69759; CAA49413.1; -.
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                                                                               SYPOAWIRII
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                                                                                                            EFETEHGEVY
                                                                                                                                                                                                        Length: 181
                                                                                                                                                                                                                                                                                                      family.
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 (Rel.
                                                                                                                                                                                                                                                                         59
                                   STANDARD;
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                                                                                                                                                                           VATRTNVTQA
                                                                               GEDNVRQVQC
                                                                                                                                            VWPPINMKKY
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181
                                                                                                                                                                                                        February 14, 2000
                                                                                                                                                                                                                                         20556
                                                                                                                                                                                                                                         MW;
                                                                                 ISFIAYKPEG
                                                                                                            DGRYWTMWKL
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RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
CHAIN 1.
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AX MEDLINE; 93144693.

AM MANZARA T., CARRASCO P., GRUISSEM W.;

PANZARA T., CARRASCO P., GRUISSEM W.;

AMANZARA T., CARRASCO P., GRUISSEM W.;

Povelopmental and organ-specific changes in DNA-protein interactions at in the tomato robes!, rbcs2 and rbcs3A promoter regions.";

RI Plant Mol. Biol. 21:69-88(1993)

CC PINCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF CC CARBOULDES 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CACAGON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENNOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH CC THE PENNOSE SUBSTRATE IN THE PHOTORESPIRATION AT THE SAME CC ACTIVE SITE.

CC ACTIVE SITE.

CC -1- CARALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 J-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

CC -1- SUBGULTULAR LOCATION: CHLOROPLAST.

CC -1- SUBGLIULAR LOCATION: CHLOROPLAST.

CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, I
15-JUL-1999 (Rel. 38, I
RIBULOSE BISPHOSPHATE C
(EC 4.1.1.39) (RUBISCO
RBCS-2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 88038372.
SUGITA M., MANZARA T., PICHERSKY E., CASHMORE A., GRUISSEM W.;
"Genomic organization, sequence analysis and expression of all
genes encoding the small subunit of ribulose-1,5-bisphosphate
carboxylase/oxygenase from tomato.";
Mol. Gen. Genet. 209:247-256(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITINE; 87163513.

MCKNIGHT T.D., ALEXANDER D.C., BABCOCK M.S., SIMPSON R.B.;

"Nucleotide sequence and molecular evolution of two tomato
encoding the small subunit of ribulose-1,5-bisphosphate
carboxylase.";

Gene 48:23-32(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PICHERSKY E., BERNATZKY R., TANKSLEY S.D., CASHMORE A.R.;
"Evidence for selection as a mechanism in the concerted ex
Lycopersicon esculentum (tomato) genes encoding the small
ribulose-1,5-bisphosphate carboxylase/oxygenase.";
Proc. Natl. Acad. Sci. U.S.A. 83:3880-3884(1986).
                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1989) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Strepto
euphyllophytes; Spermatophyta; Ma
core eudicots; Asteridae; euaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-9 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MANZARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (RBCS-2A)
MEDLINE; 86233336.
M15236; AAA34192.1; -. M13543; AAA34189.1; -. X05983; CAA29401.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
yllophytes; Spermatophyta; Magnolliophyta; eudicotyledons;
eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A. (RBCS-2).
CHERRY LA1221; TISSUE-ROOT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHERRY LA1221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
CARBOXYLASE SMALL CHAIN:
O SMALL SUBUNIT 2A) (LESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ
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5 5)
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ll subunit
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RBS2_LYCES Length:
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01-0CT-1993 (Rel. 27, La
01-0CT-1993 (Rel. 27, La
15-DEC-1998 (Rel. 37, La
RIBULOSE BISHOSPHATE CA
(EC 4.11.139) (RUBISCO S
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _SEQUENCE
RBS3_SOLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
SEQUENCE
                            PIR; S31498; S31498.
HSSP; P00866; 1RLC.
                                                                                                                                                                                                                                 ----
                                                                                                                                                                                                                                                                                                                                                         PRIIZ C.C., WOLTER F.P., SCHENKEMEYER V., HERGET T., SCHREIER P.H.;
"The gene family encoding the ribulose-(1,5)-bisphosphate
carboxylase/oxygenase (Rubisco) small submit of potato-";
Gene 137.271-274(1993).
-!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
ACTIVE STREET
                                                               EMBL; X69763; CAA49417.1;
                                                                                                                                                                                                                                                                                              +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. AM 80.5793;
MEDLINE; 94131296;
FRITZ C.C., WOLTER F.P., 9
"The gene family encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
euphyllophytes; Asteridae; euasterids I; Solanales; Solanaceae;
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PIR; S02363; RKTOS2.
HSSP, P00866; IRLC.
MENDEL; 414; LYCes; rbcS; 2.
PFAM; PF00101; RuBisCC_small; 1.
PFAM; PF00101; RuBisCC_small; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration; Photosynthesis; Carbon dioxide fixation; Chloroplast; Transit Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit
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TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solanum.
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                                                                                                                                                                                                                      ACTIVE SITE:

CAMPALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) - 2 3-PHOSPHO-D-GLYCERATE.

CAMPALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

SUBCOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

SUBCULT: B LARGE CHAINS + 8 SMALL CHAINS.

SUBCELLULAR LOCATION: CHLOROPLAST.

SUBCELLULAR LOCATION: CHLOROPLAST.

SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
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180 AA;
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180
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20278 MW;
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Last annotation update)
CARBOXYLASE SMALL CHAIN 3
O SMALL SUBUNIT 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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W: 6BE7042D CRC32;
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MENDEL; 495; SOLtu;rbcS;6 PFAM; PF00101; RuBisCO\_sm

RuBisCO\_small;

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SPETER
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!!AA_SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                            RBSK_SCHPO Length: 318
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE RIBOKINASE (EC 2.7.1.15).
SPEC16G5.02C.
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                                                                   301
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Hypothetical protein; ;
SEQUENCE 318 AA; 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL023554; CAA19022.1; PROSITE; PS00583; PFKB_KINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
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Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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TRANSIT 1 58
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                                                                                                          251
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PROSITE; PS00584; PFKB_KINASES_2;
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181
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33250 MW; D40648BF CRC32;
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Monooxygenase; Chloroplast;
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RIBULOSE BISPHOSPHATE CARBO
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PRT;

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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN
(RUBISCO SMALL SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                             REG5_DROM
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Musa acuminata (Banana).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida;
7inniberales; Musaceae; Musa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF008214; AAB63287.1; -.

PFAM; PF00101; RuBisCO_small; 1.

Photosynthesis; Carbon dioxide fixation; Photorespiration;

Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit peptide.

TRANSIT 1 58

CHLOROPLAST (BY SIMILARITY).

CHAIN 59 180

RIBULOSE BISPHOSPHATE CARBOXYLASE SMAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                        151
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  SEQUENCE FROM N.A.
STRAIN-CANTON-S; TISSUE-HEAD
MEDLINE; 96203080.
                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
RHYTHMICALLY EXPRESSED GENE 5 PROTEIN (DREG
                                                                                                                                                                                                           REG-
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CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
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                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                            protein (DREG-5)
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                                                                                                                                                                                                                                                                                                                                                             298 AA
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                                                                                                                                                     Hexapoda;
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                                                                                                                                Brachycera;
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                                                                                                                                Muscomorpha
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REG5_DROME Length: 298 February 14, 2000 08:02 Type: P Check: 7903
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-STAR MOSS; TISSUE-LEAF;

OLIVER M.J., SCOTT H.B. II;

"Desiccation-tolerance and gene expression: Analysis of a recovery clone, Tr288, and its implications in mRNA storage during drying.";

J. Exp. Bot. 45:577-583(1994).

-I. FUNCTION: ASSOCIATED WITH THE REHYDRATION EVENTS INVOLVED IN THE RECOVERY OF THE DESICCATION-TOLERANT MOSS.

-I. SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. REHYDRIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _SEQUENCE 1.0 STAN REHY_TORRU STAN P52574; 01-0CT-1996 (Rel. 01-0CT-1996 (Rel. 15-DEC-1998 (Rel.
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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"A novel circadianly expressed Drosophila melanogaster gene dependent on the period gene for its rhythmic expression.";

EMBO J. 15:1625-1631(1996).

-i- FUNCTION: INVOLVED IN THE GENERATION OF BIOLOGICAL RHYTHMS (POTENTIAL). IN THE HEAD, OSCILLATES IN ABUNDANCE WITH A DAILY PEAK DURING EARLY NUGHT, EVEN UNDER CONSTANT DARKNESS. OSCILLATION IS DEPENDENT ON PERIOD (PER) FUNCTION.

-i- TISSUE SPECIFICITY: EXPRESSED IN HEAD, BUT NOT IN THE BODY.

-i- DEVELOPMENTAL STAGE: EXPRESSED IN 24 HOURS EMBRYO.
                                             EMBL; U40818; AAA83758.1; -. HSSP; P30041; 1PRX. PF0AM; PF0AM; PF0AM; AhpC-TSA; 1.
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Antioxidant.
218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tortula ruralis (Moss).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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DOMAIN 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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32202 MW;
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24084 MW;

ADFD8F42 CRC32;

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II AA_SEQUENCE 1.0
ID REBB_NEIGO
AC P37761;
DT 01-0CT-1994 (R
DT 01-0CT-1996 (R
DT 01-0CT-1996 (R
DE DTDF-GLUCOSE 4
GN REBB.
GN REBB.
OS Neisseria gono
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RFBB_NEIGO FARTHER PROPERTY OF THE PROPERTY OF
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MEDIJINE, 81012161.

MEDIJINE, 81012161.

"Nucleotide sequence of the yeast plasmid.";

"Nucleotide sequence of the yeast plasmid.";

"Nucleotide sequence of the yeast plasmid.";

"Nature 286:860-864(1980).

-1- FUNCTION: PLASMID PARTITION REQUIRE REP1, REP2, AND A CIS-ACTING
DNA SEQUENCE (KNOWN AS STB).

DNA SEQUENCE (KNOWN AS STB).
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                                                                                                                                                                                                                                                                                          251
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EMBL; V01323; CAA24633.1;
PIR; A04504; PDBYC.
SGD; L0001612; REP2.
Plasmid; Trans-acting fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).

Plasmid 2-micron.

Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;

Saccharomycetaceae; Saccharomyces.
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STRAIN-A364A D5;
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P03872;
P1-JUL-1986 (Rel. 01, Created)
P1-JUL-1986 (Rel. 01, Last sequence update)
P1-JUL-1986 (Rel. 32, Last annotation update)
P1-JUL-1986 (Rel. 32, Last annotation update)
P1-JUL-1986 (Rel. 32, Last annotation update)
P1-JUL-1986 (Rel. 01, Created)
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296 AA; 33196 MW;
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ID RHL_MACMU

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MEDLINE; 94223693.

MEDLINE; 94223693.

MOURO I., LE VAN KIM C., CHERIF-ZAHAR B., SALVIGNOL I., BLANCHER A., CARTRON J. -P., COLIN Y.;

CARTRON J. -P., COLIN Y.;

"Molecular characterization of the Rh-like locus and gene transcripts from the rhesus monkey (Macaca mulatta).";

J. MOL. EVOL. 38:156-176(1994).

-I- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HOUSE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             028849;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
RH-LIKE PROTEIN (RHESUS-LIKE PROTEIN).
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NP_BIND 13 19 NAD (POTENTIAL).
SEQUENCE 346 AA: 38828 MW; FB9FD6A3 CRC32:
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BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
-!- SIMILARITY: STRONG, TO OTHER DTDP-GLUCOSE 4,6-DEHYDRATASES.
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PEAM; PF01370;
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                               RHO7, HUMAN STANDARD, PRT; 227 AA. 552158; 099535; 000690; 000734; 01-007-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) RHO-RELATED GTP-BINDING PROTEIN RHO7.
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A -> V (IN MAC-B).
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SEQUENCE FROM N.A.
MEDLINE; 97092865.
SMITH T.M., LEE M.K.,
HOOD L., KING M.-C.;
                                    Submitted
                                                                 HO'....
AHO7.
Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Human).
                                                         EQUENCE FROM N.A.
                                                  ISSUE-BRAIN;
                                    (FEB-1996)
                                    ö
        SZABO
                                    the
        C.I.,
                                    EMBL/GenBank/DDBJ
                                                                       Craniata; Ve: i; Hominidae;
        JEROME
        Z
                                                                         Homo
        MCEUEN M., TAYLOR M.,
                                    databases
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IIAA_SEQUENCE 1.0

II RIB7_ARCEU

AC 028272;

DT 15-DEC-1999 (1)

DT 15-DEC-1999 (1)

DT 15-DEC-1999 (1)

DT 15-DEC-1999 (1)

DE QUTATIVE 5-AM,

DE (EC 1.1.1.193

GN AF2007.1.193

GN AF2007.1.193

GN AF2007.1.193

GN AF200ENCE FROM

AF200ENCE FROM

RC AICHAROSOLE FROM

RC STRAIN=VC-16,

RA KLENK H.-P.

RA KLENK H.-P.

RA KLENK H.-P.

RA KLENK H.-P.

RA KIRKNESS E.F.

RA FLEISCHMANN M. D.

RA SADOW P.W., D.

RA SADOW P.W., D.

RA MASON T.M., CO

THE COMPLETE J.C.;

RT "THE COMPLETE

RT "THE COMPLETE

RT "THE COMPLETE

CC -! CATALYTIC

CC -! SIMILARIT

CC -! SIMILARIT
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GTP-binding; Prenylation; L
NP_BIND
NP_BIND
NP_BIND
NP_BIND
NP_BIND
119
120
NP_BIND
136
44
                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- CATALYTIC ACTIVITY: 5-AMINO-6-(5-PHOSPHORIBITYLAMINO)URACIL +
NADP(+) = 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL + NADP(+) = 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL +
-!- PATHMAY: THIRD STEP OF RIBOFLAVIN BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE HTP REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                             STRAND-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE; 98049343.

KLENK H.-P. CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.F. EXPERSON J.D., RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., DOUGHERTY B.A., MCKENLY K., ADAMS M.D., LOFTUS B. PETERSON S., REICH C.I., MCUBIL L.K., BADGER J.H., GLODEK A., ZHO OVERBEEK R., GOGAYNE J.D., WEIDMAN J.F., MCDONALD L., UTIERBACK T. COTTON M.D., SPRIGGS T., ARTIACH P., KANNE B.-P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., WASON T.M., DOLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PUTATIVE 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL
(EC 1.1.1.193) (HTP REDUCTASE)
AF2007.
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EMBL; L78833; AAC37595.1;
HSSP; P06749; 1A2B.
MIM; 601555; -.
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-i- SIMILARITY: BELONGS TO THE RHO FAMILY IN THE RAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaeoglobus fulgídus.
Archaea; Euryarchaeota; Archaeoglobales;
Archaeoglobus.
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (POTENTIAL).

GERANYL-GERANYL (BY SIMILARITY).

MW; 98964266 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVLICEDISR
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RIPA\_LUFCY Length: 277

February 14, 2000 08:02

Type:

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Check:

429

ACT\_SITE SEQUENCE SIGNAL CHAIN

179 277 ;

AA;

179 30212 MW;

ВΥ ALPHA

Y SIMILARITY. E0233100 CRC32;

PROSITE; PS00275; SHIGA\_RICIN; 1. PFAM; PF00161; RIP; 1. Antiviral; Protein synthesis inhi

Protein

synthesis inhibitor; Hydrolase; 19 277 prnon-

Toxin;

Signal.

PROTEIN LUFFIN-

20

HSSP;

P16094;

1AHB.

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RIB7_ARCFU Length: 219
                                                                                                                                                                                                                                                                                                                             MEDLINE; 92288316.

KATAOKA J. HABUKA N., MIYANO M., MASUTA C., KOIWAI A.;

"Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
inactivating protein from Luffa cylindrica.";

Plant Mol. 18:1199-1202(1992).

-I- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF THE N-GLYCOSIDIC BOND AT O
SPECIFIC ADENOSINE ON THE 28S RNA.

-I- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
PROTEINS. BELONGS TO TYPE 1 RIP.

PROTEINS. BELONGS TO TYPE 1 RIP.
                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000465;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-UTL-1992 (Rel. 38, Last annotation update)
RIBOSOME-INACTIVATING PROTEIN LUFFIN-ALPHA PRECURSOR (RRNA N-GLYCOSIDASE) (EC 3.2.2.2).
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytas; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
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                                                                                                                                                                                                                                                                                                                                     a collaboration
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RRR OCCOORDITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete amino acid sequence of luffin-b, a rib
protein from sponge gourd (Luffa cylindrica) see
Agric Biol Chem. 55:229-238(1991).

- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-
SPECIFIC ADENOSINE ON THE 28S RNA.

-! SIMILARITY: TO OTHER BACTERIAL AND PLANTS RI-
PROTEINS: BELONGS TO TYPE 1 RIP.

PROSITE: PS00275; SHIGA_RICIN; 1.

PROSITE: PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                           P24613;

01-MAR-1992 (Rel. 21, C

01-MAR-1992 (Rel. 21, I

01-OCT-1996 (Rel. 34, I

50S RIBOSOMAL PROTEIN I
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TISSUE-SEED;
MEDLINE; 9124
  SEQUENCE;
                                                                                                                                                                                                                                                                                                        SEQUENCE 1.0
RK21_SPIOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iuffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryothta; Tracheophyta;
euphyllophytas; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19,
01-AUG-1991 (Rel. 19,
15-JUL-1999 (Rel. 38,
RIBOSOME-INACTIVATING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiviral; Protein
ACT_SITE 160
SEQUENCE 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
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                                                                 Spinacia.
                                                                            Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                  151
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BY SIMILARITY. 27293 MW; 64A72993 CRC32;
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                    AND
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Last annotation update)
PROTEIN LUFFIN-B (RRNA
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seeds.";
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SEQUENCE FROM N.A.
STRAIN-CV. GEANT D'HIVER;
MEDLINE; 92025007.
LAGRANGE T., FRANZETTI B., AXELOS M., MACHE R., LERBS-MACHE S'
"Structure and expression of the nuclear gene coding for the
chloroplast ribosomal protein LD1: developmental regulation c
housekeeping gene by alternative promoters.";
Mol. Cell. Biol. 13:2614-2622(1993).
Mol. Cell. Biol. 13:2614-2622(1993).
                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 90375547.

SMOOKER P.M., KRUET V., SUBRAMANIAN A.R.;

NOTION TO THE Chloroplast

NOTION TO THE CHOROPLAST

Plant but in the nucleus in angiosperms. Isolation
protein and CDNA clone with transit and an unusual

J. Biol. Chem. 265:16699-16703(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MARTIN W., LAGRANGE T., LI Y.F.,
"Hypothesis for the evolutionary
protein L21 of spinach.",
Curr. Genet. 18:553-556(1990).
                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: THIS PROTEIN BINDS TO 23S RIBOSOMAL RNA IN THE PRESENCE OF PROTEIN L20 (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L21P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the repeat
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spinach L
sequence.
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e.";
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RK21_SPIOL Length: 256
                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                                                         EMBL; X56691; CAA40019.1; -.
EMBL; M57413; AAA34041.1; -.
EMBL; M64682; AAA74715.1; -.
PIR; S13527; S13527.
                                                                                                            TRANSIT
                                                                                                                                                  PFAM;
; $1354., A48103; A48103.

NDEL; 10833; $PIO1; rpl21; 1.

OSITE; 10833; $PIO1; rpl21; 1.

OSITE; PS00169; RIBOSOMAL_L21; 1.

PAM; PF00829; Ribosomal L21p; 1.

S5 CHLOROPLAST.

FANSIT 1 5 50S RIBOSOMAL PROTEIN L21.

HAIN 236 253 ALA/GLU-RICH.

236 253 ALA/GLU-RICH.

7 Type: P Check: 71
                 718
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щ MASATLAFSC SSLCATLKLP QNLNPLLLNV PPLSKPFSGV VSPPSLSRLS

LLPVAAKRRR FQEIPEELKA EFEEFORPPN QKPQLSDVLP DDFQAPEPGT

51

101 PEYNDIINQF EEIFAVVVIG

151 TVNDKIVLNK VLLVGTKAST YIGTPIVTNA AVHAVVEEQL LDDKVIVFKY

KKKKNYRRNI GHRQPITRIK ITGITGYEDY PASTLEAEVE

251 AEAVPV 201

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!!AA_SEQUENCE 1.0
ID RR8_MARPO
AC P06362;
DT 01-JAN-1988 (
DT 01-JAN-1988 (
DT 01-FEB-1996 (
 OGGEDDIAN
                            RPS8
 Marchantia polymorpha (Liverwort)
Chloroplast.
Eukaryota; Viridiplantae; Strepto
                                    CHLOROPLAST
Viridiplantae;
                                (Rel.
(Rel.
(Rel.
30S RJ
                                  l. 06, Crea
l. 06, Last
l. 33, Last
RIBOSOMAL
                                                                               STANDARD;
                                                             Created)
 Streptophyta;
                                    PROTEIN
                                           sequence
                                                                               PRT;
                                                                               132
 Embryophyta;
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 Marchantiopsida;
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SO WERE REPORTED TO THE PROPERTY OF THE PROPER
  RR8_MARPO
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                        GENTLES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V. Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                   STRAIN-972;
GENTLES S.,
                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 92375702.
MARKS J., SIMANIS V.;
"Cloning of the gene for ribosomal protein
Schizosaccharomyces pombe.";
Nucleic Acids Res. 20:4094-4094(1992).
                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
40S RIBOSOMAL PROTEIN S13.
RPS13 OR SPAC6F6.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
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PIR; A02716; R3LV8.
HSSP, P56309; ISEI.
MENDEL: 1315; MARPO: TPS8; 1.
PROSTITE; P500053; RIBOSOMAL_S8; 1.
PFAM; PF00410; Ribosomal_S8; 1.
Ribosomal protein; TRNA-binding; Chloroplast.
Ribosomal protein; TRNA-182; 20331A62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 322:572-574 (1986).

Nature 32:572-574 (1986).

-I--FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

-I--SIMILARITY: BELONGS TO THE S8P FAMILY OF RIBOSOMAL PROTEINS.
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This SWISS-PROT
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J. Mol. Biol. 203:333-351(1988).
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                                                                                                                           EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNEKYQGKKK
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entry is
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copyright.
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a chloroplast DNA.";
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CHANG Z.,
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                                         EMBL, L22465, AAA21916.1; -.

PROSITE; PS00548; RIBOSOMAL_S3; 1.

PFAM; PF00189; Ribosomal_S3_C; 1.

PFAM; PF00417; Ribosomal_S3_N; 1.

RIBOSOMAL PROTEIN, TRNA-BIADGING,

REDOSOMAL PROTEIN, TRNA-BIADGING,

SEQUENCE 257 AA; 28717 MW; 803552CF CRC32;
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; Z98981; CAB11741.1; --
FIR; S26296; S26296,
PROSITE; PS00362; RIBOSOMAL_
PFAM; PF00312; Ribosomal_S15
                                                                                                                                                                                                                                                                                                                                                        Phylogenetic relationships among members of the class Mollicute deduced from rps3 gene sequences."

Int. J. Syst. Bacteriol. 44:119-124(1994).

1: FUNCTION: THIS PROTEIN IS INVOLVED IN THE BINDING OF INITIATING THE BINDING OF INITIATING THE STATIAN (BY SIMILARITY).
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01-FEB-1995 (Rel. 31, Last sequence up
01-FEB-1995 (Rel. 31, Last annotation
30s RIBOSOMAL PROTEIN S3.
RPSC OR RPS3.
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INIT_MET 0
SEQUENCE 150 AA;
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  February 14,
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Acholeplasma.
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16822 MW;
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C75B8E0E CRC32;
  2000 08:02 Type:
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NHGGGKRRPS

AVSHVEIERL KELKVKKRVK ITLHSGKPGV

ALVKEDAVIR VIGREAATMK

KFLNKKYNNA

MGQKVNPIGF

RVGVIRDWDS

KWYADKKIVP

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AA_SEQUENCE 1.0

PRSB_SYNY3

AC P73307;
AC P73307;
AC P73007;
AC RIBOSOMAL PROTEIN 8.

AC RIBOSOMAL PROTEIN 8.

AC RIBOSOMAL PROTEIN 9.

AC RI
                                                                           RS8_SYNY3
(1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 96196179.
TONG J., WETMUR J.G.;
TONG J., WETMUR J.G.;
TONG J., Sequencing, and expression of ruvB and characterization of "Cloning, sequencing, and expression of thermophilic eubacteria.";
J. Bacteriol. 178:2695-2700(1996).
-I- FUNCTION: THE RUVA-RUVB COMPLEX IN THE PRESENCE OF ATP RENATURES.
CRUCTFORM STRUCTURE IN SUPERCOILED DNA WITH PALINDROMIC SEQUENCE,
INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN
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-i- FUNCTION: BINDS DIRECTLY TO THE CENTRAL DOMAIN OF 16S RIBOSOMAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus aquaticus
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11-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
10LLIDAY JUNCTION DNA HELICASE RUVB.
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cus group; Thermus
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RUVB_THETH
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NP_BIND
SEQUENCE 3
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STANDARD; PRT: 217 AA.

P26428; P76673; .

01-AUG-1992 (Rel. 23, Created)
01-NOV-1995 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
SIGMA CROSS-REACTING PROTEIN 27A (SCRP-27A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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REANNELING (BY SIMILARITY).
-!- SUBUNIT: FORMS A COMPLEX WITH RUVA.
-!- SIMILARITY: TO OTHER ATP-BINDING DNA REPAIR
                                    Biochem.
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RILEY M., COLLADO-VIDES
GREGOR J., DAVIS N.W., K
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
SMILLIE D.A., FUJITA
Submitted (XXX-1993)
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BLATTNER F.R., PLU
                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria;
                                                                      SEQUENCE OF 1-24.
MEDLINE; 92245944.
UESHIMA R., FUJITA N., ISHIHAMA A.;
"Identification of Escherichia coli proteins antibodies against region 2.2 peptide of RNA
                                                                                                                                                                   "The
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STRAIN-K12 / MG1655;
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         chem. Biophys. Res. Co
FUNCTION: NOT KNOWN.
2.2 OF RPOD AND RPOH.
SIMILARITY: BELONGS T
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                                                                                                                                                      complete genome sequence nce 277:1453-1474(1997).
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            TO THE
                                                                                                                                                                                                                                                                                  TOWNSLEY F.M., ISHIHAMA A., HAYWARD the EMBL/GenBank/DDBJ databases.
                                    Ommun. 184:634-639(1992)
CROSS-REACTS WITH ANTIE
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             FAMILY
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                                       ANTIBODIES
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                                                                        cross-reacting w
polymerase sigma
                                                                                                                                                                    coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae;
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                                                                                                                                                                                            T., BURLAND V., MAYHEW G.F., ROSE D.J.,
                                     AGAINST REGION
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A ANDERSSON S.G.E., ZOMORODIPOUR A., PODOWSKI R.M., NAESLUND A.K.,
A SICHERITZ-PONTEN T. ALSMARK U.C.M., PODOWSKI R.M., NAESLUND A.K.,
A ERIKSSON A.-S., WINKLER H.H., KURLAND C.G.;
The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
The genome sequence of Rickettsia prowazekii and the origin of rithe genome sequence of Rickettsia prowazekii and the origin of RT THE GEOMORY PROTEIN EXPORT INTERACTS WITH SECA AND SECE TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLASMA MEMBRANE,
CC TO ALLOW THE TRANSLOCATION OF PROTEINS (TY).
CC BY FORMING PART OF A CHANNEL (BY STMILARITY).
CC COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS (BY SIMILARITY).
CC COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS (BY SIMILARITY).
CC SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
CC -!- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
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                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the EUropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                    EMBL; AJ235272; CAA15079.1;
PROSITE; PS00755; SECY_1; F
PROSITE; PS00756; SECY_2; I
Protein transport; Transmem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PREPROFIN TRANSLOCASE SECY SUBUNIT.
SECY OR RE639.
Rickettsia prowazekii.
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EMBL; U18997; AAA58011.1; ALT_INIT.
EMBL; AE000400; AAC75241.1; ALT_INIT.
PIR; JN0287; JN0287.
ECOGENE; EG11383; YHBL.
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Rickettsiaceae; Rickettsieae; Rickettsia.
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195
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SECY_1; FALSE_NEG.
SECY_2; 1.
; Transmembrane; Translocation
; 37
POTENTIAL.
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FPACWFWLNE (IN REF. 1).
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transport; M 17

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ID SIXA_ECOLI
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SEQUENCE FROM N.A.
STRAIN-K12 / MC4100;
MEDINE; 98149313.
MEDINE; 98149313.
OGINO H., MATSUBARA M., KATO N., NAKAMURA Y., MIZUNO T.;
PAN Escherichia coli protein that exhibits phosphohistidine
phosphatase activity towards the HPt domain of the ArcB sens
involved in the multistep His-Asp phosphorelay.";
Mol. Microbiol. 27:573-585(1998).
SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
BLATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T.
BILATINER F.R., PLUNKETT G. III, BLOCH C.A., DERNA N.T.
BILET M., COLLADO-VIDES J., GLASSEE R.D., RODE C.K., M
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.T.
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.T.
MAU B., SHAO Y.;
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
PHOSPHOHISTIDINE PHOSPHATASE SIXA (EC 3.1.3
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                                                                                                      STRAIN-K12
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                     "The complete genome sequence of science 277:1453-1474(1997).
                                                                                                                                       Science
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Bacteria; Proteobacteria;
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137
169
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                                                                                                                                                                                                                                                                                                                                                             subdivision; Enterobacteriaceae;
                                                                                                                                                Escherichia coli K-12.";
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3.1.3.-) (RX6).
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VLKDEGVKSV

LIVSHLPLVG AGETFHQVNQ AEVMANSDKA

EIVAELYGKR NPISFYPATI AQLLWDGNKS

EIWEGITPYG AFLQGQWLKQ

HAHSVIDYLE HLSTLVINSL

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MNIFIMRHGE

RHLTVYGSKQ

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SIXA_ECOLI
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Bacteria; Pr
Haemophilus.
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 36, Last sequence
15-JUL-1998 (Rel. 36, Last annotatic
PHOSPHOHISTIDINE PHOSPHATASE SIXA HC
SIXA OR HI1338.
                                                                                                                                                                                                                                                                                                                                                                                                                   FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FIIZLEDH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDDLOM E., COTTON M.D., UTTERBACK T.R., PHILLIPS C.A., SPRIGGS T., HEDDLOM E., COTTON M.D., ETINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
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EMBL; AE00032; AAC75400.1;
EMBL; D90864; CAB22123.1; -.
EMBL; D90865; CAB22129.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as the contraction of t
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                                             EMBL; U32813; AAC22985.1; TIGR; HI1338; -.
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Virulence.

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STYGENE; SG10464; SPAL.
PROSITE; PS00152; ATPASE\_ALPHA\_BETA;
PFAM; PF00006; ATP-synt\_ab; 1.
Hydrolase; Hydrogen ion transport; AT

transport; ATP synthesis;

EMBL; U08279; AAA74038.1; EMBL; X73525; CAA51921.1; EMBL; U10872; AAA83429.1; PIR; S37304; S37304.

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SPAL_SALT
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STRAIN=SR11 / SL1344;
MEDLINE: 94321319.
MEDLINE: 94321319.
EICHELBERG K., GINCCCHIO C.C., GALAN J.E.;
"Molecular and functional characterization
"Molecular and functional characterization
typhimurium invasion genes invB and invC: h
FOPI AFPase family of proteins.";
J. Bacteriol. 176:4501-4510(1994).
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Bacteria; Proteobacteria;
                                                                                                                             This SWISS-PROT entry is copyright. between the Swiss Institute of Bio the European Bioinformatics Institute
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"Cognate gene clusters govern
Salmonella typhimurium and Shi
EMBO J. 12:3779-3787(1993).
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01-FEB-1996 (Rel. 33, Last annotation
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Spiroplasmataceae; Spiroplasma.
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STRAIN-ATCC 33219 / BC3;
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G -> A (IN REF. 2).
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February 14, 2000 08:02

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It is produced through a collaboration

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                                                SEQUENCE FROM N.A.

STRAIN-IT2:
MEDLINE, 97285756.
MEDLINE, 97285756.
MEDLINE, 97285756.
KUBO T. HOLDEN D.W.;
"Functional analysis of ssaJ and the ssaK/U operon, 13 genes encocomponents of the type III secretion apparatus of Salmonella Components of that 17 is secretion apparatus of Salmonella Pathogenicity Island 2.";
Pathogeni
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15-JUL-1998 (Rel. 36, Created)
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STRAINE; 91267949.
MEDLINE; 91267949.
EVERRIT K.D.E., HATCH T.P.;
EVERRIT K.D.E., HATCH T.P.;
"Sequence analysis and lipid modification of the cysteine-rich envelope proteins of Chlamydia psittaci 6BC.";
J. Bacteriol. 173:3821-3830(1991).
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Bacteria; Chlamydiales;
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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YAMADA Y., POST S.R., WANG K., TAGER H.S., BELL G.I., SEINO S.;

YAMADA Y., POST S.R., WANG K., TAGER H.S., BELL G.I., SEINO S.;

YCloning and functional characterization of a family of human and mouse somatostatin receptors expressed in brain, gastrointestinal tract, and kidney.",

Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).

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                                                                                                                                                                                                                                                                                    musculus (Mouse
aryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; A41795;
DB; GCR_0;
                                                                                                                                                                                                                                         L OR SMSTR1.

L OR SMSTR1.

Tyota; Metazoa; Chordata; Craniata; Vertebrata; ryota; Metazoa; Chordata; Craniata; Vertebrata; Crota; Metazoa; Chordathi; Muridae; Murinae; Craniata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDYYATALKS RAYSVEDFQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATVSQLSVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family;
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_0272; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Last sequence
Last annotation
TYPE 1 (
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annotation updat
1 (SS1R) (SRIF-2
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (P
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BY SIMILARITY.
PALMITATE (POTENTIAL).
; 28C01B27 CRC32;
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
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3 (POTENTIAL).
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS

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SSR1_MOUSE
  RRRR OCC OCC DIT DIC
                                                                                                                                                               ID SSR1_RAT
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PROSITE;
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TRANSMEM
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                                                                                    P28646;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 37, Last annotation update)
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DOMAIN
                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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STRAIN-WISTAR; TI
MEDLINE; 92096119
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                        SEQUENCE FROM N.A.
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PS00237; G_PROTEIN_RECEPTOR;
00001; 7tm_1; 1.
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family; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                            391 AA;
              TISSUE-BRAIN
                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                             LGYANSCANP
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POTENTIAL.

BY SIMILARITY.

BY ALMITATE (POTENTIAL).

BD335205 CRC32;
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CYTOPLASMIC (I
4 (POTENTIAL)
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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                                                    Mammalia;
Rattus.
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51

VPFLVTSTLL ISFIYSVVCL

RHWPFGALLC VGLCGNSMVI CGEGVCSRGP

RLVLSVDAVN MFTSIYCLTV

YVILRYAKMK

TATNIYILNL

GSGAADGMEE PGRNSSQNGT

MFPNGTAPSP TSSPSSSPGG

NSDGTVACNM LMPEPAQRWL

VGFVLYTFLM

GFLLPVGAIC LCYVLIIAKM

 VWVLSLLVIL

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SSR1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEYERHOF W., PAUST I
"Cloning of a cDNA of
receptor expressed
DNA Cell Biol. 10:61
                                                                                                                                                                                                                                                                                                                                               GCRDB; GCR_0183; --
GCRDB; GCR_0628; --
PROSITE; PS00237; G_F
PFAM; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics are no restrict. the European Bioinformatics Institute. There are no restrict: use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and forentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     G-protein
Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain.";
J. Biol. Chem.
-!- FUNCTION: I
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LI X. -J., FORTE M., NORTH R.A., ROSS C.A., SNYDER S.H.;

"Cloning and expression of a rat somatostatin receptor enriched
                                                      DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X62314; CAA44193.1;
EMBL; M97656; -; NOT_ANNO
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                                                                                                                                                                  TRANSMEM
DOMAIN
                                                                                                                                                                                                                         TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
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PIR; A45102; A45102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOXIN INSENSITIVE G PROTEINS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: BRAIN, PITUITARY, ISLET, JEJUNUM,
HEART, SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                             DOMAIN
                                                                                                                           TRANSMEM
                                                                                                                                          DOMAIN
                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                                                                   RANSMEM
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FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR SOMATOSTATIN THIS RECEPTOR IS COUPLED TO PHOSPHOTYROSINE PHOSPHATASE AND NA+/H+ EXCHANGER VIA PERTUSSIS
Length: 391 February 14, 2000 08:02 Type: P Check: 9240
                                                                                                                                                                                                                                                                                                              un coupled rece family
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CDNA encoding a novel putative G-protein-coupled
ssed in specific rat brain regions.";
10:689-694(1991).
                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                  NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                     receptor;
                                                                                                                                                                                                                                                                                                                                                             PROTEIN_RECEPTOR; 1.
                              42746 MW;
                            7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
EX SIMILARITY.
BY SIMITATE (POTENTIAL).
PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein;
                                                                                                                                                                   5 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                         GYTOPLASMIC (
                                                                                                                                                                                              4 (POTENTIAL)
EXTRACELLULAR
                                                                                                                                                                                                                                                    2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                               CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in no way
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SSRB_CANFA
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Cra
Eukaryota; Metazoa; Fissipedia;
                                                                      DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
MEDLINE;
GOERLICH
                                           CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  WADA I., RINDRESS D., CAMERON P.H., OU W.-J., DOHERRY J.J. II,
LOUVARD D., BELL A.W., DIGNARD D., THOMAS D.Y., BERGERON J.J.M.;
"SSR alpha and associated calnexin are major calcium binding proteins
of the endoplasmic reticulum membrane.";
of the endoplasmic reticulum membrane.";
1. Biol. Chem. 266:1959-19610(1991).
1. Biol. Chem. 266:1959-19610(1991).
1. BIOL. TRAP PROTEINS ARE PART OF A COMPLEX WHOSE FUNCTION IS TO
BIND CA(27) TO THE ER MEMBRANE AND THEREBY REGULATE THE RETENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 18-42;
MEDLINE; 92011761.
WADA I., RINDRESS D., CAMERON P.H., OU W.-C.
LOUYARD D., BELL A.W., DIGNARD D., THOMAS I
                                                                                                                                                                                                                     EMBL; X53529; CAA37609.1; -. EMBL; X53591; CAA37661.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOERLICH D., PREBIN S., HARTMANN E., HERZ J., OTTO A., KRAFT R., WIEDMANN M., KNESPEL S., DOBBERSTEIN B., RAPOPORT T.A.; "The signal sequence receptor has a second subunit and is part of translocation complex in the endoplasmic reticulum as probed by bifunctional respents";
J. Cell Biol. 111:2283-2294(1990).
                              SEQUENCE
                                                                                                                                             Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           OF ER RESIDENT SUBUNIT: HETEROTERAP-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                  RETICULUM.
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                                                                                                                                                                         A36679; A36679
B37273; B37273
S15510; S15510
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Length:
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                                           18
150
170
170
88
104
                                                                                                                                                                                                                                                                                                                                                                                                                          SIDENT PROTEINS.
HETEROTETRAMER OF TRAP-ALPHA,
                                                                                                                                                Signal;
 183
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. 34, Last annotation update)
IAMED PROTEIN, BETA SUBUNIT PRECURSOR (TRAP-BETA)
RECEPTOR BETA SUBUNIT) (SSR-BETA) (GP25H).
                                                         149
169
183
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February
                              20100
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                                                                                                                                                            Endoplasmic reticulum; Transmembrane
                              W.
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 14,
                                                         LUMENAL (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
                                                                                                                    TRANSLOCON-ASSOCIATED SUBUNIT.
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ia; Canidae;
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                              977848EB CRC32;
 2000
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 08:02
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e; Canis.
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Type:
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   Check:
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151
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AAFGVMTLPS
                         GYFNFTSATV TYLAQEDGPV VIGFTSAPGQ GGILAQREFD RRFSPHFLDW
IGIPLLLWYS
 SKRKYDTPKS
 KKN
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"Cloning and sequence analysis of the beta stranslocon-associated protein.";
Biochim. Biophys. Acta 1217:101-102(1994).
-i. FUNCTION: TRAP PROTEINS ARE PART OF A COBIND CA(2+) TO THE ER MEMBRANE AND THERE OF ER RESIDENT PROTEINS.
-i. SUBUNIT: HETEROTETRAMER OF TRAP-GAMMA.
TRAP-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                             P43308;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
TRANSLOCON-ASSOCIATED PROTEIN, BETA SUBUNIT P
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                               <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                             ISSUE-COLON CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                     RETICULUM.
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                                                                                                                                                                                                                             LULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR BETA SUBUNIT PRECUR RECEPTOR BETA SUBUNIT) (SSR-BETA)
                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; i; Hominidae; Homo
                                                                                                                                                                                                                                                  TRAP-ALPHA, TRAP-BETA,
                                                                                                                                                                                                                                                                                                              of the beta subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
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                                                                                                                                                                                                                                                                      COMPLEX WHOSE
EREBY REGULATE
                                                                                                                                                                                                                                                                                                                                                                                                                              PRECURSOR (TRAP-BETA)
                                                                                                                                                                                                                                ENDOPLASMIC
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                                                                                                                                                                                                                                                  TRAP-DELTA
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EMBL; This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement in not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). X74104; CAA52207.1;

CHAIN Slycoprotein; 18 Signal; Endoplasmic reticulum; Transmembrane 1 17 BY SIMILARITY. 183 TRANSLOCON-ASSOCIATED PROTEIN,

DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
CARBOHYD
SEQUENCE 18 150 170 188 104 183 AA; 149 169 183 88 20135 MW; POTENTIAL.
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
POTENTIAL. SUBUNIT LUMENAL B2E82B37 CRC32; (POTENTIAL).

SSRB\_HUMAN Length: 183 February 14, 2000 08:02 Type: ש Check:

- MRLLSFVVLA LFAVTQAEEG ARLLASKSLL NRYAVEGRDL TLQYNIYNVG
- 51 SSAALDVELS DDSFPPEDFG IVSGMLNVKW DRIAPASNVS HTVVLRPLKA
- 101 TYLAQEDGPV VIGSTSAPGQ GGILAQREFD
- 151 AAFGVMTLPS IGIPLLLWYS SKRKYDTPKT

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OC SOLUTION OCCION 
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01-NOV-1997
01-NOV-1997
01-NOV-1997
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ST14_SOLT
                                  Solanum tuberosum (Potato)
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                            STS14 PROTEIN
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7 (Rel. 35, Last sequ
7 (Rel. 35, Last anno
EIN PRECURSOR.
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Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                  sequence update) annotation update
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51  $\vdash$ 

SSAALDVELS DDSFPPEDFG MRLLASVLLA LFAVSHAEEG

IVSGMLNVKW ARLLASKSLL

DRIAPASNVS HTVVLRPLKA NRYAVEGRDL TLQYNIYNVG

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RX MEDLINE; 96197407.

RA VAN ELLINE; 96197407.

RA SCHRAUWEN J.A.M., WULLEMS G.J.;

"Molecular analysis of a pistil specific gene expressed in the stigma and cortex of Solanum tuberosum.";

"Molecular analysis of a pistil specific gene expressed in the stigma and cortex of Solanum tuberosum.";

"Plant Mol. Biol. 30:171-176(1996).

"Plant Mol. Biol. 30:171-176(1996).

"Plant Mol. Biol. 30:171-176(1996).

"PROKTION: MAY PROTECT THE OUTER TISSUES OF THE PISTIL FROM PAUROSUM ANT ANTACK.

"PARHOGEN ATTACK.

"PARHOGEN ATTACK.

"TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE STIGMA AND STYLAR CORTEX THROUGHOUT PISTIL DEVELOPMENT. NOT EXPRESSED IN OTHER CORTEX THROUGHOUT PISTIL DEVELOPMENT. NOT EXPRESSED IN OTHER CORANS.

"PARHOGEN AND INCREASES TO MARKET THE PISTIL AROUND 120 HOURS BEFORE AUTHESIS AND INCREASES TOWARDS THE END OF FLOWER DEVELOPMENT, WITH A MAXIMUM AT ANTHESIS.

"INCLEASED TOWARDS TO A FAMILY THAT GROUPS MANMALIAN SCP/TPX1;

"STMILARITY: BELONGS TO A FAMILY THAT GROUPS MANMALIAN SCP/TPX1;

"STMILARITY: BELONGS TO A FAMILY THAT GROUPS MANMALIAN SCP/TPX1;
                                                                                                                                                                                                                                                                                                          AA_SEQUENCE 1.0

SUFI_HAEIN STANDARD; PRT; 311

P44847;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence upda
15-JUL-1999 (Rel. 38, Last annotation up
SUFI PROTEIN HOMOLOG PRECURSOR.

SUFI OR HI0733.
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SIGNAL 1
CHAIN 20
REPEAT 13
DOMAIN 59
SEQUENCE FROM N.A.
STRAIN-RD / KW20;
MEDLINE; 95350630,
FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., MERRICK J.M.,
KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
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or send a
                                                                                                                                                                                                                                                    Haemophilus influenzae.
Bacteria; Proteobacteria;
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HSSP; P04284; ICFE.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; FALSE_NEG_PROSITE; PS01010; SCP_AG5_PR1_SC7_2; FALSE_NEG_PFAM; PF00188; SCP; 1.
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                                                                                                                                                                                                                         Haemophilus
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core eudicots;
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214
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23887 MW;
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STSI PROTEIN.
3.5 X 2 AA TANDEM REPEAT
POLY-PRO.
; 06BC0717 CRC32;
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IIAA_SEQUENCE 1.0 ID SUH3_RAT AC P50235;
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C STRAIN=SPRAGUE-DAWLEY; TISSUE-LIVER;

C STRAIN=SPRAGUE-DAWLEY; TISSUE-LIVER;

X MEDLINE; 94306585.

X MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

MOLECULAR Cloning and functions of rat liver hydroxysteroid

T "MOLECULAR Cloning and functions of rat liver hydroxysteroid

T polycyclic arylmethanols to DNA.";

C Chem. Biol. Interact. 92:87-105(1994).

C C.:- FUNCTION: CATALYSES SULFATION OF HYDROXYSTEROIDS AND XENOBIO

C (BY SIMILARITY).

C -:- CATALYTIC ACTIVITY: 3'-PHOSPHOADENYLYSULFATE + AN ALCOHOL =

C ADENOSINE 3'5'-SISPHOSPHATE + AN ALKYL SULFATE.

C -:- SUBCELULAR LOCATION: CYTOPLASMIC.

C --- SUBCELULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID
SULFOTRANSFERASE) (ST)
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VENTER J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
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SUFI PROTEIN HOMOLOG
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GROWTH HORMO

HORMONE

AND XENOBIOTICS

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IIAA_SEQUENCE 1.0

IID T2C1_CHVI3

AC PS2283;

AC COLUTJ.

AC COLU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and applications of the two/three-base endonuclease R.CviJI from IL-3A virus-infected C Gene 157:37-41(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 9533159/.
SKOWRON P.M., SWAMINATHAN N., MCMASTER
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(R.CVIJI).

Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
TYPE II RESTRICTION ENZYME CVIJI (EC 3.1.21.4) (ENDONUCLEASE CVIJI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE; 96292246.
                                          EMBL; U09001; AAC55064.1; -. REBASE; RB00873; CV1JI.
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of the three base restriction endonuclease R.Cviji from eukaryotic Chlorella virus II-JA.", "Nucleic Acids Res. 24:2463-2469(1996).
Nucleic Acids Res. 24:2463-2469(1996).
-i- CATALYTIC ACTIVITY: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE RGCY
-i- CATALYTIC ACTIVITY: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE RGCY
AND CLEAVES AFTER 6-2. IN THE PRESENCE OF ATP, THERE IS A RELAXATION OF ITS SPECIFICITY AND IT CAN CLEAVE RGCN AND YGCY, BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWAMINATHAN N., MEAD D.A., MCMASTER K., GEORGE D., VAN ETTEN J.L.,
                                                                                                                                                                                                                                                                                                                                                     NOT YGCR.
-!- COFACTOR: REQUIRES MAGNESIUM.
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              Restriction
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          system; Magnesium
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                                                                                                 EMBL; X59869; CAA42526.1; -.
EMBL; X59870; CAA42527.1; -.
EMBL; X59871; CAA42528.1; -.
EMBL; X63901; CAB56795.1; -.
PIR; S16645; S16645.
PIR; A38095; A38095.
TRANSFAC; T00999; -.
TRANSFAC; T01001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDITINE; 92235082.

VAN DE WETERRING M.L., OOSTERWEGEL M.A., HOLSTEGE F., DOOYES D.,

VAN DE WETERRING M.L., OOSTERWEGEL M.A., CLEVERS H.;

SUJJKERBUIJK R., GEURTS VAN KESSEL A., CLEVERS H.;

"The human T cell transcription factor-1 gene. Structure,

"The human T cell transcription factor-1.";

J. BJOL. Chem. 267:8530-8536(1992).

J. BJOL. Chem. 267:8530-8536(1992).

J. FUNCTION: TRANSCRIPTIONAL ACTIVATOR INVOLVED IN T-CELL LYMPHOCYTE

DIFFERENTIARION. IT BINDS TO THE T-LYMPHOCYTE-SPECIFIC ENHANCER

ELEMENT (5-WWCAAAG-'3') FOUND IN THE PROMOTER OF THE CD3-EPSILON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation (TCF-1)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
17-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1)
17-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1)
17-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1)
18-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1)
18-CELL-SPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE; 91114695.
VAN DE WETERING M.L., OOSTERWEGEL M.A., DOOIJES D., CLEVERS H.;
"Identification and cloning of TCF-1, a T lymphocyte-specific
transcription factor containing a sequence-specific HMG box.";
EMBO J. 10:123-132(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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-i- ALTERNATIVE PRODUCTS: THREE DIFFERENT FORMS THAT DIFFER IN THE C-TERMINAL SECTION ARE PRODUCED BY ALTERNATIVE SPLICING.

-i- TISSUE SPECIFICITY: T-CELL SPECIFIC.

-i- SIMILARITY: CONTAINS 1 HMG BOX.
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PF00505;

Nuclear protein; HMG\_box;

Transcription regulation; Activator;

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SOFTT
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
TELETHONIN (TITIN CAP PROTEIN)
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
EMBL; AJ000491; CAA04129.1; -. EMBL; AJ010063; CAA08987.1; -. EMBL; AJ011098; CAA09479.1; -.
                                                                                                                                                                                                                                                                          MUES A., GAUTEL M.;
"Structure of the human
Submitted (SEP-1998) to
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
PALLAVICINI A., VALLE G., LANFRANCHI G.;
"Human telethonin genomic sequence.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELT_HUMAN
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VARSPLIC
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                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-SKELETAL MUSCLE;

MEDLINE; 98010471.

VALLE G., FAULKNER G., DE ANTONI A., PACCHIONI B., PALLAVICINI PANDOLFO D., TISO N., TOPPO S., TREVISAN S., LAMFRANCHI G.;

"Telethonin, a novel sarcomeric protein of heart and skeletal
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the EMBL/GenBank/DDBJ databases
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ETNMPRELKDGNGQESLSMSSSSSPA -> GGKRNAFGTYP

EKRAAAPAPFLPMTVL (IN ISOFORM B).

ETNMPRELKDGNGQESLSMSSSSSPA -> DPGSPKKCRAR

FGLNQQTBMCGPUR (IN ISOFORM C).

7BB387D9 CRC32;
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IIAA SEQUENCE 1.0

ID TRAM_AGRT6 STANDARD; PRT; LC_
AC 057471;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
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070548;
15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
TELETHONIN (TITIN CAP PROTEIN)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Agrobacterium tumefaciens Plasmid pTiA6NC. Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases i- FUNCTION: MUSCLE ASSEMBLY REGULATING FACTOR. -- SUBCELULAR LOCATION: SARCOMERIC. -- SUBURIT: INTERACTS WITH TITIN.
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"The titin cap protein formation.";
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ITSSUE-DIAPERAGM;
EEVOLELLA C., FORMENTIN E., VALLE G., LANFRANG
"Skeletal muscle transcripts characterization
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                                                                                                                                                                                                                                                                                                           SQEAQRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19078 MW;
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rization in Homo sapiens
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alpha subdivision;

Rhizobiaceae

group;

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OF REAL COCCOCCOCCETTE NO.
TRAM_AGRT6 Length: 102
                                                                                                                                                                                                                                                                                  MEDLINE: 97061201.

KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., KIKANEKO T., SATO S., KOTANI H., TANAKA A., ASAMOTO S., KIMURA Y., MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T., HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YASUDA M., TABATA S.;

"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";

DNA Res. 3:109-136(1996).

DNA Res. 3:109-136(1996).
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"Activity of the Agrobacterium Ti plasmid conjugal transfer re
Trar is inhibited by the product of the tram gene.";

J. Bacteriol. 177:1367-1373(1995).

-i- FUNCTION: NEGATIVELY REGULATES CONJUGATION AND TRA GENES

-i- EXPRESSION BY ANTAGONIZING TRAR/AAI DEPENDENT ACTIVATION.

EITHER BIND OR MODIFY TRAR OR AAI MAKING THEM UNAVAILABLE.

ALTERNATIVELY, TRAM MAY BIND TRA PROMOTERS PREVENTING TRAN

ALTERNATIVELY, TRAM MAY BIND TRA PROMOTERS PREVENTING TRAN
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRNA (GUANINE-N1)-METHYLTRANSFERASE (EC 2.1.1.31)
METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 1.0
TRMD_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as lon-
modified and this statement is not remov-
entities requires a license agreement (So
or send an email to license@isb-sib.ch).
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EMBL; U16786; AAA64838.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobiaceae;
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                                                                                                                                                                                     CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE. + TRNA - S-ADENO:
L-HOMOCYSTEINE + TRNA CONTAINING N(1)-METHYLGUANINE.
SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY
                                                                                                                                                                                                                                                     (BY SIMILARITY)
CATALYTIC ACTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٧×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         February 14, 2000 08:02 Type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chroococcales; Synechocystis
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of the tram gene.";
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SON
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ID TRMU_YEAST
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13947;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE
(EC 2.1.1.61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BROWN D., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-I-CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + TRNA = S-ADENOSYL-L-
HOMOCYSTEINE + TRNA CONTAINING 5-METHYLAMINOMETHYL-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPAC23H4.04.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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Transferase; Methyltransf
                                        401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=972;
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                                                                                             NALYICRGIN
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                                                                                             NELLMSKCIY
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ID TRNH_DATST
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15-JUL-1998
15-JUL-1998
15-JUL-1998
NAKAJIMA K., HASHIMOTO T., YAMADA Y.;
"Two tropinone reductases with different stereospecificities short-chain dehydrogenases evolved from a common ancestor.";
Proc. Natl. Acad. Sci. U.S.A. 90:9591-9595(1993).
                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
TROPINONE REDUCTASE HOMOLOG (EC 1.1.1.-) (P29X).
Datura stramonium (Jimsonweed) (Common thornapple).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; Z74081; CAA98591.1; -.
Transferase; Methyltransferase; tRNA processing.
SEQUENCE 417 AA; 47049 MW; 4690E911 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAULIN L., SAREN A.M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + TRNA - S-ADENOSYL-L-HOMOCYSTEINE + TRNA CONTAINING 5-METHYLAMINOMETHYL-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROBABLE TRNA (5-
(EC 2.1.1.61).
YDL033C OR D2761.
                                                                                              TISSUE-ROOT
                                                                                                            SEQUENCE FROM N.A.
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
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SIMILARITY: BELONGS TO THE TRMU FAMILY.
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(Rel. 36, Last sequence update)
(Rel. 36, Last anotation update)
(Rel. 36, Last anotation update)
AN (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                        STANDARD;
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TRNH_DATST Length: 268 February 14, 2000 08:02 Type:
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EMBL; M74901; AAA51445.1; -.
PIR; JN0451, JN0451.
HSSP; Q56320; INSJ.
PFAM; PF00218; IGPS; 1.
PFAM; PF00697; PRAI; 1.
Isomerase; Tryptophan biosynthesis.
PEQUENCE 312 AA; 33070 MW; C5A4F8A8 CRC32;
                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restricted by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-or.send.an.email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 93083987.
                                                                                                                                                                                                                                                                                                                                                                              Cryptococcus neoformans (Filobasidiella neoformans)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tre
                                                                                                                                                                                                                                                                                                                                                                                                                   Ol-AUG-1992 (Rel. 23, Created)
Ol-AUG-1992 (Rel. 23, Last sequence update)
Ol-AUG-1994 (Rel. 29, Last annotation update)
Ol-G'-PHOSPHORIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24) (PRAI).
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HSSP; P19992; 2HSD.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; Adh_short; 1.
PFAM; PF00678; Adh_short_C2; 1.
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FAMILY (SDR)
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167
268 AA;
                                                                                                                                                                                                                                                                                                                                                                   ngi; Basidiomycota;
Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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MEDLINE; 96034516.
VAN RENTERGHEM P.H.G.,
"Study of TTF-1 gene e:
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1)
(HOMEOBOX PROTEIN NKX-2.1)
                                                                                                                                                                                                                                                                                                                                                                 EMBL; X77910; CAA54868.1;
HSSP; P23441; 1FTT.
                                                                                                 SEQUENCE
                                                                                                                                                                                               DNA_BIND
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FUNCTION: TRANSCRIPTION RACTOR THAT BINDS AND ACTIVATES THE FUNCTION: TRANSCRIPTION SPECIFIC GENES SUCH AS THYROGLOBULIN, PROMOTER OF THYROID SPECIFIC GENES SUCH AS THYROCLOBULIN. THE THYROID DIFFERNTIATION PHENOTYPE. MAY PL MAINTENANCE OF THE THYROID DIFFERNTIATION PHENOTYPE. MAY PL ROLE IN LUNG DEVELOPMENT AND SURFACTANT HOMEOSTASIS.
SUBCELLULAR LOCATION: NUCLEAR.
SUBCELLULAR LOCATION: NUCLEAR.
SINGLARTY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
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                                                                                                                                                                                                                                               Activator; Homeobox; DNA-binding;
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QDTMRNSASG PGWYGANPDP

TAAGVPQLSH RFPAISRFMG

PASGMNMSGM

GGLGSLGDVS

51

AAMQQHAVGH

HGAVTAAYHM

SAVGGYCNGN

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SEQUENCE FROM N.A.
MEDLINE; 95229626.
IKEDA K., CLARK J.C., '
WHITSETT J.A.;
WHITSETT J.A.;
"Gene structure and ex
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P4369; 01495; 014954;

01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
THYROLD TRANSCRIPTION FACTOR 1 (THYROLD NUCLEAR FACTOR 1) (TTF-1)
(HOMEDON PROTEIN NEXX-2.1).
TITF1 OR NEXX2A.
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                                                                        ENDO T., OHNO M., NAKAZATO M.;
Submitted (MAY-1995) to the EMBL/Genbank/DDBJ databases.

-i- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVATES THE PROMOTER OF THYROID SPECIFIC GENES SUCH AS THYROGLOBULIN, THYROFEROXIDASE, AND THYROTROPIN ROBEPTOR. CRICIAL IN THE MAINTENANCE OF THE THYROID DIFFERENTIATION PHENOTYPE. MAY PLAY ROLE IN LUNG DEVELOPMENT AND SUBFACTANT HOMEOSTASIS.

-i- SUBCELLULAR LOCATION. NUCLEAR.

-i- TISSUE SPECIFICITY: THYROID AND LUNG.
-i- SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-LUNG;
HAMDAN H., LIU H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-THYROID;
MEDLINE; 95226464.
SAIARDI A., TASSI V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                   TISSUE-LUNG;
HAMDAN H., LIU H., JONES
Submitted (OCT-1995) to t
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Submitted (JAN-1996)
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Submitted (JAN-1995)
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e EMBL/GenBank/DDBJ
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IIAA_SEQUENCE 1.0
IID TTF1_MOUSE
AC P50220;
DT 01-0CT-1996 (R
DT 01-0CT-1999 (R
DT 01-0CT-1999 (R
DT 10-0CT-1999 (R
DT 11-7UL-1999 (R
DE THYROLID-TRANSC
DE (HOMEDBOX PROT
GN TIF1 OR TTF1
OS Mus musculus (C Eukaryota; Met
OC Eukaryota; Met
OC Eukaryota; Met
OC Eukaryota; Met
OC EURACYOTA; Met
OC EURACYOTA; Met
OC EUROCE FROM
RF STRAIN-129/SF,
RX MEDIANE; 9522(
RA OGUCHI H., PAN
RT "The Complete
RT enhancer -bind:
RT deduced amino
RL Biochim. Biop)
CC -1-FUNCTION:
CC THYROPEGO;
CC MAINTENAN(
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EMBL; V19816; AAC50125.1; -.
EMBL; U19756; AAR86099.1; -.
EMBL; U3203; AAR89066.1; ALT_INIT.
EMBL; U33749; AAR852381.1; -.
EMBL; D50740; BAA23529.1; -.
EMBL; D50740; BAA23527.1; -.
EMBL; D50739; BAA23527.1; -.
EMBL; D50739; BAA23527.1; -.
EMBL; D50740; BAA23527.1; -.
STRAIN-129/SV; TISSUE-LIVER;

MEDLINE; 95226463.

OGUCHI H., PAN Y.T., KIMURA S.;

OGUCHI H., PAN Y.T., KIMURA S.;

OGUCHI H., PAN Y.T., KIMURA S.;

"The complete nucleotide sequence of the mouse thyroid-specific enhancer-binding protein (T/EBP) gene; extensive identity of the deduced amino acid sequence with the human protein.";

Biochim. Biophys. Acta 1261:304-306(1995).

-I- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVATES THE PROMOTER OF THYROID SPECIFIC GENES SUCH AS THYROGLOBULIN, THYROFEOXIDASE, AND THYROTROFIN RECEPTOR. CRUCIAL IN THE MAINTENANCE OF THE THYROID DIFFERENTIATION PHENOTYPE. MAY PLAY A
                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1996 (Rel. 38, Last annotation update)
THYROID-TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1)
(HOMEDBOX PROTEIN MKX-2.1).
TITF1 OR TITF1 OR NKX2-1 OR NKX-2.1.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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an email to license@isb-sib.ch).
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HOMEOBOX.
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H -> P (IN REF. 6).
S -> T (IN REF. 6).
R -> G (IN REF. 6).
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QQ -> HE (IN REF. 5).
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SEQUENCE
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DI LAURO R.;
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STANDARD;

P23441; 008630; 070121;

01-NOV-1991 (Rel. 20, Created)

101-NOV-1991 (Rel. 20, Last sequence update)

15-UIL-1999 (Rel. 38, Last annotation update)

THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR (HOMEDOX PROTEIN NKX-2.1).

TITF1 OR TTF1 OR TTF-1 OR NKX-2.1.

TITF1 OR TTF1 OR TTF-1 (THYROID NUCLEAR (HOMEDOX PROTEIN NKX-2.1).
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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-! SUBCELLULAR LOCATION: NUCLEAR.
-! TISSUE SPECIFICITY: THYROLD, LUNG AND BRAIN.
-! SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
-! SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
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E047C32A CRC32;
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(TTF-1) gene.";

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ID TXF8_DENAN
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"Structural study of rat thyroid tra (TTF-1 HD) by nuclear magnetic reson FEBS Lett. 336:397-402(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. [3]
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                                              301
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EMBL; D38035; BAA07231.1; ALT_SEQ.
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                           Transcription regulation;
Nuclear protein; 3D-struct
DNA_BIND 161 220
                                                                                                                                                                                                                                                                                                    TRANSFAC; T00856;
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                                                                                                                                                                                                                                                                                 PROSITE
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                             LNSSGSDYGA
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                                                                                                       KNMAPLPSAP
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372 AA;
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                                                                                                       RRKRRVLFSQ
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                                                                                                                                                                                                                                          3D-structure
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                                                                                                                                                                                                      38554 MW;
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                                               QPGSAGQSPD
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POLY-ALA.
AE0F1572 CRC32;
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resonance.";
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                                                                                                                                                                                                                                                             Homeobox; DNA-binding;
                                               LAHHAASPAA
                                                                 ASLQGHAQQQ
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IIIAA_SEQUENCE 1.0
ID UBC7_DROME
AC P52487;
DT 01-0CT-1996 (F
DT 01-0CT-1996 (F
DT 01-NOV-1997 (F
DE UBIQUITIN-CONN
DE LIGASE) (UBIQU
GN UBC84D;
OS Drosophila mel
OC Eukaryota; Met
OC Ephydroidea; I
RN [1]
RP SEQUENCE FROM
RA ROBIN C., MEDV
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DISULFID
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21-JUI-1986 (Rel. 01, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAFB).
Dendroaspis angusticeps (Eastern green mamba),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae;
                                                                                                             LIGASE) (UBIQUITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentialities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Venom;
SIGNAL
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VILLOEN C.C., BOTES D.P.;
VILLOEN C.C., BOTES D.P.;
VILNOEN C.C., BOTES D.P.;
VILNOEN C.C., BOTES D.P.;
VILNOEN C.C., BOTES D.P.;
VILNOEN TAB From Dendroaspis angusticeps venom.";
VILNOEN TAB FROM DENDROSPIS ANGUSTON IS UNKNOWN.
VILLOEN TABLE TO THE PHARMACOLOGICAL ACTION IS UNKNOWN.
                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A01675; T5EP2A.
PIR; S211299; S211299.
HSSP; P01416; INTX.
PROSITE; PS00272; SNAKE_TOXIN;
PFAM; PF00087; toxin; 1.
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TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-VENOM GLAND;
DUCANCEL F.;
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                                                                                                                                                                                                                                                                                                                                                         Length: 81
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A
                                                                                                                                                                                                              STANDARD;
                                                                                                                      CARRIER PROTEIN)
                                                                                                                                                                                                                                                                                                               February
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EOBFC94E CRC32;
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                                                                                                                                  update) (EC 6.3.2.19) (UBIQUITIN-PROTEIN
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                                                            Hexapoda; Ins
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                                                               Muscomorpha;
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SEQUENCE FROM N.A.
ROBIN C., MEDVECZKY

X.M.,

RUSSELL R.J.,

OAKESHOTT

J.G

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01-NOV-1986
01-NOV-1986
15-JUL-1999
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HSSP; P15731; 2UCE.
FLYBASB: FB990017456; Ubc84D.
PROSITE: PS00183; UBIQUITIN_CONJUGAT;
PFAM; PF00179; UQ_con; 1.
Ub19U1111 conjugation; Ligase.
UB1QUITI
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE; 85242679;
MEDLINE; 85242679;
KITAGAWA Y., AKABOSHI E., SHINAGAWA H., HORII T., ON

"Structural analysis of the umu operon required for

mutagenesis in Escherichia coli.",

Proc. Natl. Acad. Sci. U.S.A. 82:4336-4340(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coll.
Proteobacteria;
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SEQUENCE FROM N.A.
STRALIN=K12 / M61655;
MEDLINE; 97426617
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMUD_ECOLI P04153;
                                                                                                                                                                                                                                                          MEDLINE; 85242678.

MEDLINE; 85242678.

MITCHELL B.B., MARSH L., PERRY K.L., ELEDGE S.J., MITCHELL B.B., MARSH L., TURNEY WILL B.B., MARSH L., TURNEY WILL B.B., MARSH L., MITCHELL B.B., MITCHELL B.B., MARSH L., MITCHELL B.B., MITCHELL B.B., MARSH L., MITCHELL B.B., MARSH L., MITCHELL B.B., 
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 85242678.
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(Rel. 03, Last sequence update)
(Rel. 38, Last annotation update)
N (EC 3.4.21.-) [CONTAINS: UMUD' p)
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41698C20 CRC32;
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                                                                                                                                                                                                                                                             , MARSH L., WALKER G. are required for UV MucA, and LexA prote
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EMBL; M10107; AAAA98073 1; -
EMBL; AE000216; AAA78673 1; -
EMBL; D90752; BAA36030.1; -
EMBL; D90753; BAA36038.1; -
PIR; A03551; ZWECD.
PIR; A03551; ZWECD.
PIR; A035157; AZ2157;
PDB; 1DWU; 01-AUG-96.
PDB; 1AV9; 28-JAN-98.
ECO2DBASE; A01551; UMUD.
ECOGENE; EG11057; UMUD.
ECOGENE; EG11057; UMUD.
SOS mutagenesis; DNA repair; Autocatalytic cleserine protease; 3D-structure.
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MUTAGEN
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MUTAGEN
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MEDLINE; 92318898.
MEDLINE; ENNIS D.G.,
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MEDLINE; 97061202.
MEDLINE; 97061202.
OSHIMA T., AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A.,
OSHIMA T., AIBA H., BABA T., FUJITA K., HAYASHI K., KASHIMOTO K.,
INADA T., ITOH T., KAJIHARA M., KANAI K., KASHIMOTO K.,
KIMURA S., KITAGAWA M., MAKINO K., MASUDA S., MIKI T., MIZOHUCHI K.,
MORI H., MOTOMURA K., NAKANURA Y., NASHIMOTO H., NISHIO Y., SAITO N.,
SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y.,
YANO M., HORIUCHI T.;
'A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                  PROPER
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilb-sib.ch).
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[4]
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-I- FUNCTION: INVOLVED IN UV PROTECTION AND MUTATION. ESSENTIAL FO INDUCED (OR SOS) MUTAGENESIS. MAY MODIFY THE DNA REPLICATION MACHINERY TO ALLOW BYPASS SYNTHESIS ACROSS A DAMAGED TEMPLATE.

-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 324 ALSO KNOWN AS THE UMUD/LEXA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96202734.
PEAT T.S., FRANK E., MCI
HENDRICKSON W.A.;
"Structure of the UmuD'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF UMUD'.
MEDLINE; 96202734.
MEDLINE; 96202734.
MEDLINE; PRANK E., MCDONALD J.P., LEVINE A.S.,
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    MW;
UMUD' PROTEIN.

CLEAVAGE (AUTO-).

INVOLVED IN AUTO-CLEAVAGE.

INVOLVED IN AUTO-CLEAVAGE.

P->D: IN UMUD1; NON-CLEAVABLE.

G->R: IN UMUD1; NON-CLEAVABLE.

G->D: IN UMUD7; NON-CLEAVABLE.

MW; D0175DFA CRC32;
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UMUD\_ECOLI

51

TYFVKASGDS MIDGGISDGD LLIVDSAITA SHGDIVIAAV DGEFTVKKLQ

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Length: 139

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February

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SEDTLDVFGV VIHVVKAMR

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STREET BROOKS BEEFFER RESERVED SONS BEEFFER BROOKS 
ROCCOSSEDER
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AC Q06240;
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01-OCT-1993
01-JUN-1994
01-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLLE C.F. III, FLOWERS C.C., O'CALLAGHAN D.J.;
"Open reading frames encoding a virus, and a novel glycoprotein glycoprotein gar of pseudorables virus, and a novel glycoprotein within the unique short segment of equine herpesvirus type 1.";
Virology 188:545-557(1992).

-i. SIMILARITY: BELONGS TO THE HERPESVIRUSES US2 FAMILY.
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PIR; A44215; A44215.
CONFLICT 31 31
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SENSOR PROTEIN VANS (EC 2.7.3.-) (VANCOMYCIN (VANCOMYCIN HISTIDINE PROTEIN KINASE).
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                                              Plasmid pIP816.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                   Enterococcus
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[Arology 191:649-660(1992)]
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EDLINE; 93079867.
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(Rel. 29, Last sequence update)
(Rel. 33, Last annotation update)
                                                                                                      faecium (Streptococcus faecium).
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33502 MW;
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839D6C1D CRC32;
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P36778;
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SEQUENCE
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-!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM VANS/VANR.

-!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM VANS/VANR.

ACTIVATES THE TRANSCRIPTION OF VANH, VANA AND VANX IN RESPONSE TO VANCOMYCIN WHICH RESULTS IN VANCOMYCIN RESISTANCE. VANS ACTIVATES VANR BY PHOSPHORYLATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.
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ARTHUR M., MOLINAS C., COURVALIN P.;
The VanS-VanR two-component regulatory system controls synthesis depsipeptide peptidoglycan precursors in Enterococcus faecium EM4147.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARTHUR M., MOLINAS C., DEPARDIEU F., COURVALIN P.;
"Characterization of In1946, a In3-related transposon conferring
glycopeptide resistance by synthesis of depsipeptide peptidoglycan
precursors in Enterococcus faccium BM4147.";
J. Bacteriol. 175:117-127(1993).
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                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
REGULATORY PROTEIN E2.
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EMBL; M68910; AAA24788.1; -.
PFAM; PF00512; signal; 1.
Sensory transduction; Transferase; Kinase; Transmembrane; Cell
Antibiotic resistance; Phosphorylation; Plasmid.
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                                          Human papillomavirus type
Viruses; dsDNA viruses ""
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384 AA;
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164
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                                                   Papovaviridae;
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PIR; S36552; S3652.
HSSP; P17383; 1DHM.
PFAM; PF00508; EZ_N; 1.
PFAM; PF00511; EZ_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SEQUENCE 383 AA; 44246 MW; CFBD1DEA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
DELIGY H. HOFMANN B.;

PETIDES H. HOFMANN B.;

PETIDES H. HOFMANN B.;

CUIT. TOP, MICIOSIOL. Immunol. 186:13-31(1994).

CUIT. TOP, MICIOSIOL. Immunol. 186:13-31(1994).

IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCUNUNUNGGT-3') PRESENT IN MULTIPLE COPIES IN THE REGULATION REGION. IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
REGULATORY PROTEIN E2.
                                                                                                                                                                                                                                                                                                              VE2_HPV10
P36781;
                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 94265501.
                                                                                                                                                                                                    Human papillomavirus type 1
Viruses; dsDNA viruses, no
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SUBUNIT: BINDS DNA AS A DIMER.
SUBCELLULAR LOCATION: NUCLEAR.
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                                                                                                                                                                                                                  papillomavirus
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o RNA stage; Papovaviridae;
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ID VE2_HPV18
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MEDLINE; 87283882.
COLE S.T., DANOS O.;
"Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses repeated structure of the E6 and E7 gene products.";
J. Mol. Biol. 193:599-608(1987).
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PIR; S36535; S36535.
HSSP; P17383; 1DMM.
PFAM; PF00508; E2_N; 1.
PFAM; PF00511; E2_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding; Transcription regulation; Repressor; Nuclear protein SEQUENCE 376 AA; 43003 MW; 799683D3 CRC32;
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+ +
                                             "TAGI is a single out enzyme for HPV-18.";

Nucleic Acids Res. 21:1041-1041(1993).

-i- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE E2RE RESPONSE ELEMENT (5'- ACCHNININGGT-3') PRES

IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN ETHER

ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DN
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P06790;
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MEDLINE; 93197132.
MEISSNER J.;
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
REGULATORY PROTEIN E2.
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SUBCELLULAR LOCATION: NUCLEAR.
 REPLICATION.
SUBUNIT: BINDS DNA AS
SUBCELLULAR LOCATION:
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es; dsDNA viruses, no R
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 NUCLEAR.
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and the EMBL outstation

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PIR; D26251; W2ML18.
HSSP; P17383; 1DHM.
PFAM; PF00508; EZ_N; 1.
PFAM; PF00511; EZ_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SEQUENCE 365 AA; 41294 MW; 1871C1FE CRC32;
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a clother the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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use by non-profit instruction modified and this statement is not remove modified and this statement agreement ('
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                                                                                                                                                                                                     EMBL; U31783; AAA79425.1;
HSSP; P17383; 1DHM.
PFAM; PF00508; E2_N; 1.
PFAM; PF005511; E2_C; 1.
SEQUENCE 376 AA; 43234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
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101
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                                                                                                                                                      Length: 376
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28; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
PROTEIN E2.
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NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIRSCH-BEHNAM A., DELIUS H., DE VILLIERS E.M.;

"A comparative sequence analysis of two human papillomavirus (HPV)

"A comparative sequence analysis of two human papillomavirus (HPV)

types 2a and 57.";

"Virus Res. 18:81-98(1990).

"Virus Res. 18:81-98(1990).

"IT BINDS TO THE EZRE RESPONSE ELEMENT (5'-ACCUNNNUNGGT-3') PRESENTIN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER ACTIVATE OR REPRESS IN THE REGULATION OF EZRE'S POSITION WITH REGREDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of hicinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
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PFAM; PF00538; E2_N; 1.

PFAM; PF00518; E2_C; 1.

PFAM; PF00511; E2_C; 1.

Early protein; Transcription regulation; Activator; DNA-binding; Transcription; Peprication; Repressor; Nuclear protein.

SEQUENCE 391 AA; 43233 MW; BJDF7AF6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 91188699.
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)1-MAY-1992 (Rel. 22, Last seq
L5-yUL-1998 (Rel. 36, Last ann
EEGULATORY PROTEIN E2.
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'iruses; dsDNA viruses, no RNA stage; Papovaviridae;
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                                                                                                                     SVSSTQASAS
                                                                                                                                                                                                                                              MWDAPPKKCW KKKGQSVLVK FDGSSDRDMI YTSWGFIYVQ DTITDSWHKV
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RWGHGDTDSV
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email to license@isb-sib.ch)
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annotation
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VE2_HPV31
P17383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J04353; AAA46953.1; -.
PIR; D32444; W2WL31.
PDB; 1DHM; 07-DEC-96.
PFAM; PF00508; EZ_N; 1.
PFAM; PF00511; EZ_C; 1.
PFAM; PF00511; EZ_C; 1.
Transcription regulation; Activator; DNA-binding;
Trans-acting factor; DNA replication; Repressor; Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-II- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

-II BLINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCUNUNUNGGT-3') PRESENT IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER ACCTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INTITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
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LIANG H., PETROS A.M., MEADOWS R.D., YOON H.S., EGAN D.A., WIHOLZMAN T.F., ROBINS T., FESIK S.W.;

"Solution structure of the DNA-binding domain of a human "solution structure of the DNA-binding domain of a human papillomavirus E2 protein: evidence for flexible DNA-binding papillomavirus E2 protein:
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GOLDSBOROUGH M.D., DISILVESTRE
GOLDSBOROUGH M.D., DISILVESTRE
"Nucleotide sequence of human p
neoplasia-associated virus.";
Virology 171:306-311(1989).
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01-AUG-1990 (Rel.
15-JUL-1998 (Rel.
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SUBUNIT: BINDS DNA AS A DIMER.
SUBCELLULAR LOCATION: NUCLEAR.
DDFLNTVKIP
                                                                                                                                                                                                                                                                                                                                                                                                              METLSQRLNV CQDKILEHYE
                                                      DANILKCLRY
                                                                                                                                                                                                                                                                                             LYLTAPIGCL
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NTVSVSTGYM
                                                      RLSKYKQLYE
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15, Last sequence update)
36, Last annotation update)
N E2.
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۲ RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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ROCORDIDAC
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                                          VEZ.HPV51 SIANUAL...
P26547;
01-AUG-1992 (Rel. 23, Cr)
01-AUG-1992 (Rel. 23, Lr)
15-UTU-1998 (Rel. 36, L)
15-UTU-1998 (Rel. 36, L)
Human papillomavirus type 5 Viruses; dsDNA viruses, no [1]
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PIR; S36564; S36564.
HSSP; P17383; DLHM.
PFAM; PF00508; E2_N; 1.
PFAM; PF00511; E2_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding;
Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SEQUENCE 368 AA; 41946 MW; 7D4616A6 CRC32;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
REGULATORY PROTEIN E2.
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MEDLINE; 94265501.
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Last sequence up
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           RNA stage; Papovaviridae; Papillomavirus.
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VE2_HPV51
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01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
15-JUL-1998 (Rel.
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LUNGU O. CRUM C.P., SILVERSTEIN S.J.;

**Biologic properties and nucleotide sequence analysis of human

papillomavirus type 51.";

J. virol. 65:4216-422(1991).

-i- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

-i- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

-i- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION IT CAN EITHER

IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER

ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
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PIR; B40415; W2WL51.
HSSP; P17383; 1DLM.
PFAM; PF00508; E2_N; 1.
PFAM; PF00511; E2_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein; SEQUENCE 358 AA; 40908 MW; E0C9694E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
MEDLINE; 91303675
                                                                                                                SEQUENCE FROM N.A. MEDLINE; 94265501.
                                                                                                                                                                                                           REGULATORY PROTEIN
                                                                                                   DELIUS H., HOFMANN B.;
                                                                                                                                                              Human papillomavirus type !
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
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LAR LOCATION: NUCLEAR.
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36,
129,
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                                                                                                                                                                Papillomavirus
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NGGT-3') PRESENT
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VE2_HPV52
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01-OCT-1993
01-OCT-1993
01-OCT-1994
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                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsend an email to license@isbsib.ch).
                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 94018622.
MEDLINE; 94018625., POWERS S., ROSENBERG M.;
WULFF D.L., HO Y.S., POWERS S., ROSENBERG M.;
The int genes of bacteriophages P22 and lambda are regulated different mechanisms.";
MOI. Microbiol. 9:261-271(1993).
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PFAM; PF00508; E2_N; 1.

PFAM; PF00511; E2_C; 1.

Early protein; Transcription regulation; Activator; Early protein; Transcription regulation; Repressor; Nuc SEQUENCE 368 AA; 41739 MW; 918AE9D9 CRC32;
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HSSP; P17383; 1DHM.
 EMBL; L06296; AAC18882.1;
PIR; S35282; S35282.
SEQUENCE 317 AA; 35719
                                                                                                                                                                                                                                                            Bacteriophage P22.
Viruses; dsDNA viruses,
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VEAA_BPP22
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clear protein
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VEAA\_BPP22

Length: 317

35719 MW; 0 February 14,

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Check: 7758

05933D59 CRC32; 1, 2000 08:02 T

MITITKERIE

LFVKSPLENG LTRGEQMELA RIALASLDAE TVRYLNKFSG

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WCKENNA R., BOWMAN B.R., IIAG L.L., ROSSMANN M.G., FANE B.A.,
"Atomic structure of the degraded procapsid particle of the
bacteriophage 64: induced structural changes in the presence of
calcium ions and functional implications.";
J. Mol. Biol. 256:736-750(1996).
I-FUNCTION: MAJOR SPIKE COMPONENT. INVOLVED IN THE ACTEACHMENT TO
THE BACTERIAL HOST.
I-SUBUNIT: THE VIRION IS COMPOSED OF 60 COPIES EACH OF THE F. G.
J PROTEINS, AND 12 COPIES OF THE H PROTEIN. THERE ARE 12 SPIKES
WHICH ARE EACH COMPOSED OF 5 G AND ONE H PROTEINS.
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MEDLINE; 79053264.
MEDLINE; 79053264.
GODSON G.N., BARRELL B.G., STADEN R.,
"Nucleotide sequence of bacteriophage
Nature 276:236-247(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MAJOR SPIKE PROTEIN (G PROTEIN) (GPG).
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                                        EMBL; J02454; AAA32324.1; --
EMBL; V00657; CAA24020.1; --
EMBL; M25080; AAA32328.1; --
PIR; A04252; ZGBPC4,
PDB; 1GFF; 03-APR-96.
                                                                                                                           use by non-prefit institutions as lone modified and this statement is not remove entitles requires a license agreement (SG or send an email to license@isb-sib.ch).
                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Site-specific initiation of a DNA fragment: nucleotide sequence the bacteriophage G4 negative-strand initiation site."; Proc. Natl. Acad. Sci. U.S.A. 75:3094-3098(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; /8248/33.
SIMS J., DRESSLER D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                Coat protein;
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-81 FROM N.A.
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27
177 AA;
                       03-APR-96.
in; 3D-structure.
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 18820
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G4 DNA.";
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REF. 2).
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VGG\_BPG4

Length:

177

February

14,

2000

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Type: P

Check: 4484

51

TTHSGLCHVV

MFQKFISKHN APINSTQLAA TKTPAVAAPV LSVPNLSRST ILINATTTAV

RIDETNPTNH HALSIAGSLS NVPADMIAFA IRFEVADGVV

A U

USEQUENCE 1.0
VGLM\_HSVSA
Q01017;

STANDARD;

PRT;

366 AA

! AA

301

201 251

IQIAIPASII

AFVFLGSCIC

FIHRCQRRYR

RPRGQIYNPG

351

TPGASRPTPP
SRHRLTVAQV
GVSCAVNEAA
GPVVLLSVSP

RPRSGPTAPQ

MARLGAELRS HPNTPPKPRR RSSSSTTMPS LTSIAEESEF

151

VLGVALSANG

TFVYNGSDYG

SCDPAQLPFS

APRLGPSSVY

101

MPGRSLQGLA ILGLWVCAIG LVVRGPTVSL VSDSLVDAGA VGPQGFVEED LRVEGELHEV GAQVPHTNYY DGIIELFHYP LGNHCPRVVH VVTLTACPRR PAVAFTLCRS THHAHSPAYP TLELGLARQP LLRVRTATRD YAGLYVLRVW

RTTTPPSSPR DPTPAPGDTG

TPAPASGEIA PPNSTRSASE

51

VGLI\_HSV2H

Length: 372

February 14, 2000 08:02 Type: P Check:

501

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P13291;
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VGLI_HSV2H
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                                                                                  EMBL; X04798; CAA28485.1; -. EMBL; Z86099; CAB06714.1; -. PIR; F43674; F43674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus (type 2 / strain
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
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01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                  Submitted (FEB-1997)
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         MCGEOCH D.J., MOSS H.W.M., MCNAB D., FRAME M.C.;
"DNA sequence and genetic content of the HindIII I region in the
short unique component of the herpes simplex virus type 2 genome:
identification of the gene encoding glycoprotein G, and evolutionary
comparisons.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 87111457.
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                                                                        ycoprotein.
                                                                                                                                                                                                                                                                                                                                                                        Gen. Virol. 68:19-38(1987).
                                                                                                                                                                                                                                                   MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 2: GH, GB, GC, GG, GI, AND GE.
SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GPIAND TO PRV GP63.
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156
169
175
243
372 AA;
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 156
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39558 MW;
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Herpesviridae;
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SOT TITITIES OF REAL PROPERTY OF THE PROPERTY 
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01-APR-1993
01-OCT-1996
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TRANSMEM 18
TRANSMEM 87
TRANSMEM 152
TRANSMEM 214
TRANSMEM 236
                                                                                                                                                 01-AUG-1990 (Rel. 15, 001-NOV-1990 (Rel. 16, 01-NOV-1990 (Rel. 16, VIRB8 PROTEIN.
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DOMAIN
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1.0
VIB8_AGRT5
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J. Virol. 66:5047-5058(1992).
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Viruses; dsDNA viruses, no F
                        Agrobacterium tumefaciens.
Plasmid pTiC58.
Bacteria; Proteobacteria; alpha
Rhizobiaceae; Agrobacterium.
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                                                               subdivision;
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                                                               Rhizobiaceae group;
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MEDLINE; 90301800.

ROGOWSKY P.M., POWELL B.S., SHIRASU K., LIN T.-S.,
ROGOWSKY P.M., POWELL B.S., KADO C.I.;

"Molecular characterization of the vir regulon of
tumefaciens: complete nucleotide sequence and gene
the 28.63 kbp regulon cloned as a single unit.";
L Plasmid 23.85-106(1990).

L Plasmid 23.85-106(1990).

C -i- FUNCTION: VIRB PROTEINS ARE SUGGESTED TO ACT
C -i- FUNCTION: THERE PLAY AN IMPORTANT ROLE IN D
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P09781;
MEDLINE; 90:
WARD J.E., I
NESTER E.W.
J. Biol. Ch
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Agrobacterium tume...
Plasmid pTiA6.
Bacteria; Proteobacteria; al
Bacteria; Agrobacterium.
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01-AUG-1991 (Rel.
15-DEC-1998 (Rel.
VIRB8 PROTEIN.
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MEDLINE; 90318324.

KULDAU G.A., DE VOS G., OWEN J., MCCAFFREY G., ZAMBRYSKI P.;

"The virb operon of Agrobacterium tumefaciens pTiC58 encodes reading frames.";

Mol. Gen. Genet. 221:256-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crown gall tumor; Plasmid.
CONFLICT 21 22
CONFLICT 128 129
SEQUENCE 237 AA; 26294 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X53264; CAA37361.1; EMBL; J03320; AAA91598.1; PIR; S12348; B8AG58.
                                                                                                                                  WARD J.E., AKIYOSHI D.E., REGIER D., NESTER E.W.;
"Characterization of the virB operon tumefaciens Ti plasmid.";
J. Biol. Chem. 263:5804-5814(1988).
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                                                                                         REVISIONS.
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                                      90170994.
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26294 MW;
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SA -> TR (IN REF. 2);
CD671958 CRC32;
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ID VIB8_AGRT9
AC P05357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens.
Plasmid pT115955.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Agrobacterium.
[1]
EMBL; X06826; CAA29978.1; ALT_INIT. PIR; S00784; B8AG55. Crown gall tumor; Plasmid. SEQUENCE 230 AA; 25408 MW; 870AF438 CRC32;
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Analysis of the complete nucleotide sequence of the Agrobacterius tumefaciens virb operon.";
Nucleic Acids Res. 16:4651-4636(1988).
-i- FUNCTION: VIRB PROTEINS ARE SUGGESTED TO ACT AT THE BACTERIAL SURFACE AND THERE PLAY AN IMPORTANT ROLE IN DIRECTING T-DNA TRANSFER TO PLANT CELLS.
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01-AUG-1991 (Rel. 19, Last sequence update)
01-AWY-1992 (Rel. 22, Last annotation update)
VIRB8 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THOMPSON D.V., MELCHERS L.S., IDLER K.B., HOCYKAAS P.J.J.;
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PIR; I28621; B8AGA6.
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RP SEQUENCE FROM N.A.

RY MEDLINE, 89039712.

RA HERYMAN I., MURANAKA I., OKA A.;

RA HERYMAN I., MURANAKA I., OKA A.;

RA HERYMAN I., MURANAKA I., OKA A.;

RT MOTOGRATIZATION and characterization of the virCD genes from

RT MOTOGRATIZATION AND A TUMBERGIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERGIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERGIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERGIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERGIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERGIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERGIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERGIENS A SITE

CC AND INTEGRATION OF A DEFINED SEMENT (T.DNA) OF TI PLASMID DNA

CC SPECIFIC ENDONUCLEASE THAT CLEAVES AT A UNIQUE SITE WITHIN BOTH

CC 24 BP DIRECT REPERSIS FLANKING THE T-DNA.

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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
T-DNA BORDER ENDONUCLEASE VIRD1 (EC 3.1.-.-).
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Plasmid pRiA4b.
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VID1\_AGRRA Length: EMBL; X12867; CAA31350.1; -.
PIR; S06883; S06883.
Hydrolase; Nuclease; Endonuclease; Crown gall tumor; Hydrolase; T-DNA. 147 AA; 147 February 14, 2000 08:02 Type: P Check: 16005 MW; 414FDDA0 CRC32;

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MSQGSKPTSS DIAINQRVGA TVEGFRVVST RLRSAEYESF SHOARLLGLS

51 DSMAIRVAVR RIGGFLEIDA ETRHKMEAIL LSIGTLSSNI AALLSAYAEN

!!AA\_SEQUENCE 1.0 PTMDLEALRA ERIAFGESFA DLDGLLRSIL SVSRRRIDGC STANDARD; 147

p18591; p06520;
01-JAN-1988 (Rel. 06, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
T-DNA BORDER ENDONUCLEASE VIRD1 (EC 3.1.-.) Agrobacterium tumefaciens.

Bacteria; Proteobacteria; alpha Rhizobiaceae; Agrobacterium. Plasmid pricsa.

subdivision; Rhizobiaceae

AC OOG OF THE REPORT OF THE RE SEQUENCE FROM N.A.

MEDLINE; 90301800.

ROGOWSKY P.M., POWELL B.S., SHIRASU K., LIN T.-S.,

ZYPRIAN E.M., SIECK T.R., KADO C.I.;

"Molecular characterization of the vir regulon of P
tumefaciens: complete nucleotide sequence and gene
the 28 63-kbp regulon cloned as a single unit.";

Plasmid 23:85-106(1990). Agrobacterium e organization ۳.

MOREL

LRESYDADTA QYAYDLVSNF SAPTVRQDYQ QFFNYPNPSS

IATMVPLSRL VPVYLWIRPD GTVDSEVSIS RLPATQEEAV VNASLWEYVR

VIB8\_AGRT9 Length: 230

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HYKEVEAFQT

ARAKSARRLS

KIIAAVAAIA

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February 14, 2000 08:02 Type: P Check:

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[2]
PRELIMINARY SEQUENCE F
MEDLINE; 85190558.
HAGIYA M., CLOSE T.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     _SEQUENCE 1.0
VID1_AGRT6
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EMBL; M11311; AAA98365.1; ALT_SEQ.

EMBL; M33673; AAA22110.1;

PIR; A22666; A22666.

PIR; S11838; S11838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WANG K., HERRERA-ESTRELLA A.H., VAN MONTAGU M.M.;
Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.

-i- FUNCTION: TUNGR FORMATION BY A.TUNEFACIENS INVOLVES THE TRANSFER
-i- AND INTEGRATION OF A DEFINED SEGMENT (T-DNA) OF TI PLASMID DNA
INTO THE PLANT NUCLEAR GENOME. THE VIRD DOPRON ENCODES A SITE-
SPECIFIC ENDONICLEARS THAT CLEAVES AT A UNIQUE SITE WITHIN BOTH
24 BP DIRECT REPEATS FLANKING THE T-DNA.
JAYASWAL R.K., VELUTHAMBI K., GELVIN S.B., SLIGHTOM J.L.;

"Double-stranded cleavage of T-DNA and generation of single-stranded T-DNA molecules in Escherichia coli by a virD-encoded border-specific endonuclease from Agrobacterium tumefaciens.";

J. Bacteriol. 169:5035-5045(1987).

J. FUNCTION: TUMOR FORMATION BY A.TUMEFACIENS INVOLVES THE TRANSFER AND INTEGRATION OF A DEFINED SEGMENT (T-DNA) OF TI PLASMID DNA INTO THE PLANT NUCLEAR GENOME. THE VIRD OPERON ENCODES A SITE-
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Plasmid pTIA6NC.
Bacteria; Proteobacteria; al
Rhizobiaceae; Agrobacterium
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                                                                                                                                                                     "The virD operon of Agrobacterium endonuclease."; Cell 47:471-477(1986).
                                                                                                                                                                                                                  YANOFSKY M.F., PORTER S.G., NESTER E.W.;
                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1989 (Rel. 12, Last annotation update)
T-DNA BORDER ENDONUCLEASE VIRD1 (EC 3.1.-.).
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VLF1\_NPVOP

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DKELKTIREK

EKNEMLKNAI

DTILNFIDSK IKLMNSDYVH

DRGLIRGAIV

SASRFEHVFD
IKIIFSLVEE
KETLQLTINF

YTNAMNLPEF

LATDRORCTP ADLONPAYDL

DREFDSVEFQ

51

Length: 374
MDGLGVRNET TF1
KYMFPKPFAP TT1

TTLKSYKSRL

February 14, 2000 08:03 Type: P Check:

889

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IIAA_SEQUENCE 1.0

ID VLF1_NPVOP

AC O10330;

DT 01-NOV-1997 (F

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RM MEDLINE; 97271

RA AHRENS C.H.; F

RA ROHRANN G.H.; F

RA ROHRANN G.H.; F

CC -1- FUNCTION:

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SQ SEQUENCE 370
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SEQUENCE FROM N.A.
AHRENG C.H., RUSSELL R.R., FUNK C.J., EVANS J., HARWOOD S.,
ROHRMANN G.F.;
"The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01030;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VERY LATE EXPRESSION FACTOR 1.
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               polyhedrosis virus genome.";
Virology 229:381-399(1997).
-!- FUNCTION: INVOLVED IN VERY LATE GENE ACTIVATION (BY SIMILARITY).
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EMBL; M17989; AAA22113.1;
PIR; A29826; A29826.
PIR; A25063; A25063.
     EMBL; U75930; AAC59079.1; -
PFAM; PF00589; Phage_integrase; 1.
Transcription regulation.
SEQUENCE 374 AA; 43165 MW; C56
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Nuclease; Endonuclease; Crown gall tumor;
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          C560AOFD CRC32;
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01-APR-1993 (Rel. 25,
01-APR-1993 (Rel. 25,
MATRIX GLYCOPROTEIN M
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T. Virol.
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PIR: JO1482; WMNZBA.

MATTIX PROTEIN; Envelope protein; Glycoprotein.

CARBOHYD 54 54 POTENTIAL.

CARBOHYD 89 89 POTENTIAL.

CARBOHYD 89 89 POTENTIAL.

CARBOHYD 186 AA; 21351 MW; CC402395 CRC32;
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Sequence analysis of M2 mRNA of bovine respiratory syncytial virus obtained from an F-M2 dicistronic mRNA suggests structural homology with that of human respiratory syncytial virus.";
J. Gen. Virol. 73:737-741(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine respiratory syncytial virus (strain A51908) (BRS)
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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P04545;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
MATRIX GLYCOPROTEIN M2 (ENVELOPE-ASSOCIATED 2
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                                                                                                      ELANGO N., SATAKE M., VENKATESAN S.;
"mRNA sequence of three respiratory syncytial virus genes encoding
two nonstructural proteins and a 22K structural protein.";
y. virol. 55:101-110(1985).
                                                                                                                                                                                                                                                                                                  Human respiratory syncytial virus (strain A2).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                         SEQUENCE FROM N.A. MEDLINE; 85135082.
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EDLINE; 85237684.
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VMA2_HRSVA Length: 194 February 14, 2000 08:03 Type: P
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EMBL; U50362; AAB86655.1; -.
EMBL; U50363; AAB866677.1; -.
EMBL; U5044; AAC55971.1; -.
PIR; A04034; WMNZ22.
Matrix protein; Envelope protein; Glycoprotein.
CARBOHYD 89 89 POTENTIAL.
CARBOHYD 191 191 POTENTIAL.
SEQUENCE 194 AA; 22154 MW; 59973F8C CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The envelope-associated 22K protein of human respiratory syncytial virus: nucleotide sequence of the mRNA and a related polytranscript.";

7. Virol. 54:65-71(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 95266253.

CONNORS M., CROWE J.E. JR., FIRESTONE C.Y., MURPHY B.R., COLLINS P.L.;

CONNORS M., CROWE J.E. JR., FIRESTONE C.Y., MURPHY B.R., COLLINS P.L.;

"A cold-passaged, attenuated strain of human respiratory syncytial

virus contains mutertions in the F and L genes.";

virology 208:478-484(1995).
                                                         SEQUENCE FROM N.A.
MEDLINE; 95088607.
ALANSARI H.M., POTGIETER L.N.D.;
"Molecular cloning and sequence analysis
"molecular cloning and sequence analysis
nucleocapsid protein, matrix protein and
ovine respiratory syncytial virus.";
J. Gen. Virol. 75:3597-3601(1994).
                                                                                                                                                                            Ovine respiratory syncytial virus (strain WSU 83-1578) (
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MURPHY B.R.;
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                                                                                                                                                                                                                                                    MATRIX GLYCOPROTEIN M2.
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                                                                                             of the phosphoprotein, 22K (M2) protein of the
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I I AA SEQUENCE 1.0 STAN
ID VMEM_LVX STAN
AC P27331;
DT 01-AUG-1992 (Rel. 2
DT 01-AUG-1992 (Rel. 2
DT 01-OCT-1994 (Rel. 3
DE HYPOTHETICAL 11.8 K
OS LLLY virus X.
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MEDLINE; 92013948.
LEVAY K., ZAVRIEV S.;
"Nucleotide sequence and gene organization of the 3'
of chrysanthemum virus B genomic RNA.";
J. Gen. V1rol. 72:2333-2337(1991).
J. Gen. V1rol. 72:2333-2337(1991).
J. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
J. SIMILARITY: TO ORF3 PROTEIN FROM POTEXVIRUSES AN
PROTEIN FROM BSMY RNA 2BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          PFAM; PFUL.
Transmembrane.
10
172
72
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CARBOHYD 54 54 POTENTIAL.
CARBOHYD 89 POTENTIAL.
                                                                                                                                                                                                                                                                                                                 EMBL; S60150; CAB31868.1; -. PIR; JQ1248; JQ1248.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus
[1]
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01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
11.4 KD MEMBRANE PROTEIN (ORF 3)
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PF01307; Plant_vir_prot; 1.
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               23, Created)
23, Last sequence up
30, Last annotation
KD PROTEIN (ORF 3).
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21133
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POTENTIAL.
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CD7955FA CRC32;
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ND TO THE 14 KD
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VMEM_LVX
                                         Transmembrane.
TRANSMEM 77
TRANSMEM 77
SEQUENCE 108
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"Partial nucleotide sequence of potato virus M RNA shows similarities to protexviruses in gene arrangement and the encoded amino acid sequences.";
J. Gen. Virol. 70:1861-1869(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 90218039:
MEDELINE; 10218039:
MEMELLINE; 90218039:
MEMOLOGIES OF C.I.M., LINTHORST H.J.M.,
MEMELINE; 10218039:
MEMOLOGIES Detween the genomes of a carlavirus (lily symptomless
virus) and a potexvirus (lily virus X) from lily plants.;
J. Gen. Virol. 71:917-924(1990).
J. GEN. VIROL. 71:917-928(1990).
J. GEN. VIROL. 71:917-928(1990).
PROTEIN FROM CARLAVIRUSES.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 89293091.
                                                                                                                                                                                                                                                                                                                                                          p17527;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
12 KD MEMBRANE PROTEIN (ORF 3).
Potato Virus M (Strain Russian) (PVM).
Viruses; SSRNA positive-strand viruses, no DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1.0
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EMBL; D14449; BAA03341.1; EMBL; X53062; CAA37234.1; PIR; PN0003; WMVYP2.
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72
108 AA;
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92
11767
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POTENTIAL.
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VSDA OR SPV
Salmonella
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 SEQUENCE FR
MEDLINE; 91
KRAUSE M.,
"Molecular
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TRANSMEM
SEQUENCE
                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
VIRGLENCE GENES TRANSCRIPTIONAL ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M12921; AAA32358.1; PIR; A23368; VHBPF6. Nucleocapsid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCGRAW T., MINDICH L., FRAN "Nucleotide sequence of the bacteriophage phi 6: novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage phi-6.
Viruses; dsRNA viruses;
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01-APR-1988 (Rel.
01-JAN-1990 (Rel.
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PIR; ;
PFAM;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                         SEQUENCE 1.0
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J. Virol. 58:142-151(1986).
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MEDLINE; 86144085.
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C54333; C54333.
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FROM N.A.
91251759.
4., ROUDIER C.,
lar analysis of
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73
109 AA;
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 TIERER J., HARWOOD J.,
the virulence locus of
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E58BC570
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 GUINEY D.;
the Salmonella dublin
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II AA_SEQUENCE 1.0
ID VRPR_SALTY
AC P13041;
DT 01-JAN-1990 (F
DT 0
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VRPR_SALDU Length: 297
SEQUENCE FROM N.A.
MEDLINE; 92041614.
CALDWEEL A.L., GULIG F.A.;
The Salmonella typhimurium virulence plasmid regulator of a plasmid-encoded virulence gene.
J. Bacteriol. 173:7176-7185(1991).
                                                                                                                                                                                                                                                                                       STRAIR-1275 WILD TYPE;
STRAIR-1275 WILD TYPE;
MEDLINE; 90016881.
PULLINGER G.D., BAIRD G.D., WILLIAMSON
"Nucleotide sequence of a plasmid gene
salmonellas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P13041;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last seque
15-DEC-1998 (Rel. 37, Last annot
VIRULENCE GENES TRANSCRIPTIONAL
MKAC OR SPVR OR VAGA.
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PROSITE; PS00044; HTH_LYSR_FAMILY; 1.

PFAM; PF00126; HTH_1; 1.

Plasmid; Virulence; Transcription reg
DNA_BIND
21 40
H-T-H MO
SEQUENCE 297 AA; 33849 MW; DA8449
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MEDLINE; 90060335.

TAIRA S., RHEN M.;

"MOLECULar organization of genes constituting the viru determinant on the Salmonella typhimurium 96 kilobase FEBS Lett. 257:274-278(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium.
Plasmid 96 kb virulence
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3, Last sequence update)

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40 H-T-H MOTIF (POTENTIAL).
33849 MW; DA84490B CRC32;
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ID WN11_CHICK
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MEDLINE: 91244158.

TAIRA S., BAUMANN M., RIIKONEN P., SUKUPOLVI S., RHEN M.,

"Amino-terminal sequence analysis of four plasmid-encoded
associated proteins of Salmonella typhimurium.",

FEMS Microbiol. Lett. 61:319-323(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE; 95298011.
TANDA N., OHUCHI H., YOSHIOKA H., NOJI S., NOHNO T.
ACHICKEN WITT Gene, WITT-11, is involved in dermal
A chicken Witt gene, Witt-11, is involved in dermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION
                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                P49339;
01-FEB-1996 (Rel. 33, Last sequence up
01-CT-1996 (Rel. 34, Last annotation
01-CT-1996 (Rel. 34, Last annotation
WNT-11 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X16111; CAA34244.1; -. PIR; S06089; S06089. PIR; S06670; S06670.
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                                                                                                             SEQUENCE FROM N.A.
MEDLINE: 96063018.
TANDA N., KAWAKAMI Y., SAITO :
"Cloning and characterization
                                                                                                                                                                                                                                                                                                       WNT11 OR WNT-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00044; HTH_LYSR_FAMILY; PFAM; PF00126; HTH_1; 1
                                                                                                                                                                     Biochem.
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: POSITIVE REGULATOR FOR THE PLASMID-ENCODED VIRULENCE FACTORS SPVA, SPVB, AND SPVC.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                             cyo.";
Seq. 5:277-281(1995).
FUNCTION: MAY PLAY A ROLE IN
BOTH LIMB AND FEATHER BUDS.
DIAMETERS.
SUBCELLULAR LOCATION: POSSIBLY EXTRACELLULAR MATRIX.
TISSUE SPECIFICITY: EXPRESSED
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297 AA;
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KTSNGSDSCD

TELIYLQSSP YMDKVVERCH

CKYHWCCYVT

YLSATKVVHR SHGTQDRQCN CKKCERTVER

RDIALDLKNK

201 251

LKASLEMKCK PMGTRKYLVP

CHGVSGSCSI KDIDIRPVKE

KTCWKGLQEL

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WN11_CHICK Length: 354 February 14, 2000 08:03
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SEQUENCE
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                                                                                                                                                                                                  EMBL; D31901; BAA06699.1; -. PROSITE; PS00246; WNT1; 1. PFAM; PE00110; WNT; 1.
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                      101
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 GYRWGGCADN
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                       LLDLERGTRE
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                                                                  AFLSLILQTG
LNYGLIMGSK
                       SAFVYALSAA
                                             SNLELMOTII
                                                                                                                                                        ; Glycoprotein; Sig
4 POTENTIAL.
4 WNT-11 PROT
9 POTENTIAL.
                                                                                                              WW:
                                            QAAREVIKTC
                                                                   ICYGIKWIAL
 FSDAPMKMKK
                       AISHTIARAC
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: 14039075 CRC32;
                                                                                                                                     POTENTIAL.
                                                                                                                                                                      PROTEIN
                                                                                                                                                                                         Signal
                                             RKTFSDMRWN
                                                                  SKTPSSLALN QTQHCKQLEG
 SGSQANKLMH
                       TTGDLPGCSC
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 LHNSEVGRQV
                        GPIPGETPGP
                                             CSSIELAPNY
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Usage

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WN11_HUMAN
O96014;
15-JUL-1999 (Rel. 38, Crea.)
15-JUL-1999 (Rel. 38, Last.)
15-JUL-1999 (Rel. 38, Last.)
15-JUL-1999 (Rel. 38, Last.)
WNT-11 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                   PRAM; PROULLY WILL, Signal.

Developmental protein; Glycoprotein; Signal.

SIGNAL 24 POTENTIAL.

CHAIN 25 354 WNT-11 PROTEIN.

CARBOHYD 40 POTENTIAL.

CARBOHYD 90 POTENTIAL.

CARBOHYD 300 90 POTENTIAL.

CARBOHYD 300 POTENTIAL.

CARBOHYD 304 304 POTENTIAL.

SEDUENCE 354 AA; 39457 MW; 3FC9C358 CRC32;
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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EMBL; X13843; CAA74159.1;
EMBL; X13844; CAA74159.1;
EMBL; X13845; CAA74159.1;
EMBL; X13846; CAA74159.1;
EMBL; X13847; CAA74159.1;
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Eukaryota; Metazoa; (
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(Rel. 38, Last sequence update)
(Rel. 38, Last annotation update)
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WN11_MOUSE STANDARD; PRT; 354 AA.

P48615;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
WNT-11 PROTEIN PRECURSOR.

WNT11 OR WNT-11.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mus.
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WILKINSON D.G., WAINWRIGHT B.G.;
WALKINSON D.G., WAINWRIGHT B.G.;
Warrine Wart-11 and Wart-12 have temporally and spatially restricted
expression patterns during embryonic development.";
Mech. Dev. 51:341-350(1955).
Hech. Dev. 51:341-350(1955).
Hech. Dev. 51:341-350(1955).
HOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMSTERS.
IS SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX.
IS SUBCELLULAR STAGE: EXPRESSED DURING EMBRYOGENESIS.
SIMILARITY: BELONGS TO THE WAT FAMILY.
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; X70800; CAA50070.1; -.
MGD; MGI:101948; WNTI1.
PROSITE; PS00246; WNTI; 1.
PFANA; PF00110; Wnt; 1.
Developmental protein; Glycoprotein; Signal SIGNAL 1 24
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WN11_MOUSE Length: 354
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  _DROME
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SEQUENCE FROM N.A.

MEDLINE; 95171909.

GRABA Y., GIESELER K., ARAGNOL D., LAURENTI P., MARIOL M.-C.,

BERENGER H., SAGNIER T., PRADEL J.;

"DWnt-4, a novel Drosophila Wnt gene acts downstream of homeotic complex genes in the visceral mesoderm.";

Development 121:209-218(1995).

1- FUNCTION: ACTS DOWNSTREAM OF HOMEOTIC COMPLEX GENES IN THE VISCERAL MESODERM AND IS REQUIRED FOR EMBRYONIC SEGMENTATION.

-I- SUBCELLULAR LOCATION: SECRETED (PROBABLE).

-I- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
WNT-4 PROTEIN PRECURSOR (DWNT-4).
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                                                                                                                                                                                             EMBL; L25316; AAA67470.1; --
FLYBASE; FB90010453; Wnt4.
PROSITE; PS00246; WNT1; 1.
PFAM; PF00110; Wnt; 1.
                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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  Length: 389
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389 AA;
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2000 08:03 Type:
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AGLAKLGIIV

AGGQGLPGNL GYGGTMLNGG GVGGAAGMGI

Eutheria; Primates;
[1]

Eukaryota; KIAA0040

Sapiens (Human). Sapiens (Human). ryota; Metazoa; Chordata; Craniata; Vertebrata; ryota; Primates; Catarrhini; Hominidae; Homo.

Q15053; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) HYPOTHETICAL PROTEIN KIAA0040.

Y040\_HUMAN

STANDARD;

153

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SWILSARRAR IVMHCWNMYV

NRPHNYFPFC QOKETRRKPN CVYYDNEMKK

ROTGOTONVS

RLIFQHKRRA

RARNITHTLL METEKEYDTA

EEEEHESNMR GALTMLALLA

CVGCRMEVRH

DEPTVFNQNQ

HVPVLDALIR HHDRQSLCWS GVVVQEYEVH

151

DANAIRTDLN

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MAGSCWLLFV VFQPQIHKNG

51

INLSHLAAFL

LGPYVLATIT

WAMYKMLLCY

KGLEMRSNFY

MKTVVALAHL

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MLVQVNYFLQ LVLHAALFGL CSFAFVFALM ATVTARYAFL LELEDSAHSI

201

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Y021_NPVOP Length: 298 February 14, 2000 08:03
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                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 34.7 KD PROTEIN (ORF19).
Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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                               EMBL; U75930; AAC59018.1; -. Hypothetical protein. SEQUENCE 298 AA; 34666 MW
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                                                                                                                                                                                                               "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
virology 229:381-399(1997).
-i- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        010280;
                                                                                                                                                                                                                                                                                          AHRENS C.H., RUSSELL R.R., FUNK C.J., EVANS J., HARWOOD ROHRMANN G.F.;
                                                                                                                                                                                                                                                                                                                                                                           Nucleopolyhedrovirus.
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298 AA; 34666 MW; 9D51A0D9 CRC32;
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Type: P Check:
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Y209_MYCGE
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MEDLINE; 9
FRASER C.M
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01-FEB-1996
15-DEC-1998
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MEDLINE: 96051387.

MEDLINE: 96051387.

MOMURA N., MITAJIMA N., SAZUKA T., TANAKA A., KAWARABAYASI Y.,

SATO S., NAGASE T., SEKI N., ISHIKAWA K.-I., TABATA S.;

"Prediction of the coding sequences of unidentified human genes. I.

The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by

analysis of randomly sampled CDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                    sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- SIMILARITY: BELONGS TO THE RLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRASER C.M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A., FLETSCHMANN R.D., BULT C.J., KERLEYAGE A.R., SUTTON G., KELLEY J. KERICHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FURRMANN NGUYEN D.T., OTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S., PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                              SEQUENCE OF 125-243 FROM N.A.
STRALN-ATCC 33530 / G-37;
MEDLINE; 94075230.
PETERSON S.N., HU P.-C., BOTT K.F., HUT
"A SURVey of the Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE; 96026346.
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153 AA; 1
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(Rel. 37, Last annotation
L PROTEIN MG209.
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                                                                                                                         FAMILY OF PSEUDOURIDINE SYNTHASES
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                                                                                                                                                                                                                                                   C.A. III;
by using :
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TON G., KELLEY J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPNQQGPHTP
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Y209_MYCGE
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EMBL; U02214; AAD12509.1; -.
TIGR; MG209; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                     P75485;

101-NOV-1997 (Rel. 35, Created)

101-NOV-1997 (Rel. 35, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation updat

HYPOTHETICAL PROTEIN MG209 HOMOLOG.
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STRAIN-ATCC 29342 / M129;
MEDLINE; 97105885.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01129; PSI_RLU; 1. PFAM; PF00849; YABO; 1. PFAM; PF01479; S4; 1.
                        EMBL; AE000053; AAB96191.1; PROSITE; PS01129; PSI_RLU; 1 PFAM; PF00849; YABO; 1. PFAM; PF01479; S4; 1.
                                                                                                                                                                                                                                                                                                                                                              Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
SEQUENCE 3
                                                                                                                                                                                                                                         pneumoniae.
                                                                                                                                                                                                                                                                  HERRMANN R.
                                                                                                                                                                                                                                                                                HIMMELREICH R.,
                                                                                                                                                                                                                                                                                                                                                   Mycoplasmataceae;
                                                                                                                                                                                                                            Nucleic Acids
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                                                                                                                                                                                                                                                     Complete sequence analysis of the genome
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                                                                                                                                                                                                 leic acids Res. 24:4420-4449(1996).
SIMILARITY: BELONGS TO THE RLU FAMILY OF PSEUDOURIDINE SYNTHASES.
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308 AA; 34996 MW;
            protein
AA.
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 35228 MW;
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3375E3F5 CRC32;
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Length: 309

February 14, 2000 08:03

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MEQTESVTTA

QRLDTFLATL

LNLSRVKVAK LIVDGLVSVN

VQPEDRVHVN WSEELFEKVP VEVQPYDFPL DILYEDEQIM VVNKPNGLIS

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01-OCT-1996 (Rel. 34, Created, 01-OV-1997 (Rel. 35, Last sequence up 01-NOV-1997 (Rel. 35, Last annotation ""POTHETICAL PROTEIN MG280.
                                                                                                 15-JUL-1999
15-JUL-1999
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRASER C.M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A., FLEISCHMANN R.D., BULT C.J., KERLAVAGE A.R., SUTTON G., KELLEY J.M., FRITCHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRMANN J.L., NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M., TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCLER T.S., PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
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FRASER C.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                  HYPOTHETICAL TP0373.
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TRANSMEM
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STRAIN-ATCC 33530
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pallidum.
Spirochaetales;
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265 AA;
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(Rel. 38, Last sequence update)
(Rel. 38, Last annotation update)
L PROTEIN TP0373.
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; 29566 MW;
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  Spirochaetaceae;
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Y373_TREPA Length: 477
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SEQUENCE FROM N.
STRAIN-NICHOLS;
MEDLINE; 9833277
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P75172;
                                                            "Complete sequence a pneumoniae."; nucleic Acids Res. 2
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE RNA HELICASE MG425 HOMOLOG.
MYCOPLASMA pneumoniae.
Bacteria; Firmicuttes; Bacillus/Clostridium .
Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE; 97105885.
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Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
-!- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
-!- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
-!- SIMILARITY: TO OTHER "BOX FAMILY HELICASES.
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                                                                                                                                                                               HIMMELREICH R.,
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SIMILARITY: BELONGS TO THE UPF0072 (MESJ/YCF62) FAMILY
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                                                                                                                                       of the bacterium Mycoplasma
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R EMBL; AE000022; AAB95867.1; -.
JR PFAM; PF00270; DEAD; 1.
JR PFAM; PF00271; helicase_C; 1.
JR PFAM; PF00271; helicase_C; 1.
JR PFAM; PF00271; helicase_C; 1.
JR PFAM; PF00271; DEVD BOX.
157 DEVD BOX.
157 DEVD BOX.
157 A4 MW; 4D9D6B21 CRC32;
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Y464_MYCGE STANDARD; PRT; 3

P47702;

01-0CT-1996 (Rel. 34, Created)

01-0CT-1996 (Rel. 34, Last sequence up

01-0CT-1996 (Rel. 34, Last annotation

HYPOTHETICAL PROTEIN MG464.
                                                                                                                                                                                                                                                                                                                                                                             SQUENCE FROM N.A.

SQUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE; 96026346.

MEDLINE; 96026346.

FRASER C. M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,

FRITCHMANN R.D., BULT C.J., KERLAVAGE A.R., SUTTON G., KELLEY J.M.,

FRITCHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRMANN J.L.,

RIGUEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M.,

TOMB J.F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,

PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).

"I SUBLELIULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                          EMBL: U39728; AAC72484.1;
EMBL; U39733; AAB01654.1;
TIGR; MG464; -.
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MPLNLNKKHK ELKTIFNPFW

LKNLKKAWGI

EIGYNFGTTG PIMYATRVPL

> DYRYDLQSNN IFKVLKVAIF

ILSLIVLLFL VRLITIVITL NSTLALEKMN EVQGKLAEIN AKYKGALDLQ

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                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE; 97105885.
HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN MG464 HONOLOG.
MYCOPlasma pneumoniae.
Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae." ;
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P75112;
                                                                                                                                                                                                                               EMBL; AE000017; AAB95810.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: TO A M.CAPRICOLUM HOMOLOG.
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February 14, 2000 08:03
                                                                      Transmembrane.
59 POTENTIAL.
70 POTENTIAL.
42 POTENTIAL.
290 POTENTIAL.
290 POTENTIAL.
291 POTENTIAL.
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D341F781 CRC32;
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                                                          CRC32;
  Type:
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                                                                                                                               P55661;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb.gor.send an email to license@isb.sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE Y4EK
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HSSP; P14061; IPDV.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "MOLEcular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-i-SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
-i-SIMILARITY: BELONGS TO BACTERIAL 'YDFG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein;
NP_BIND 8 3;
ACT_SITE 147 14;
SEQUENCE 248 AA; 20
                                                                 Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alph
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SEQUENCE FROM N.A
                                             Rhizobiaceae;
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NAD OR NADP (BY SIMILARITY).

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6679 MW; A7C5BF45 CRC32;
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TRANSMEM 64
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                                       SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., REICH C.I., SUTTON G.G., BLAKE J.A., FITZEBALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., STITEBBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus tannacht!"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q57926;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
pUTATIVE 2-ISOPROPYLMALATE/HOMOCITRATE SYNTHASE MJ0503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license egreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSEN PERREIT X.;

"MOISCULIAR DASIS OF SYMBIOSIS between Rhizobium and legumes wature 387:394-401(1997).

-I. FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT SYSTEM Y4TEFCH FOR AN ANINO ACID. PROBABLY RESPONSIBLE TRANSLOCATION OF THE SUBSTRAIE ACROSS THE MEMBRANE.

"IS SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y503_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
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Hypothetical
jannaschii.";
Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000098; AAB91860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                  ethanococcus.
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SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGGIYLILTI VASALVRIVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG PF00528; BPD_transp; 1. mino-acid transpert; Amino-acid transpert;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
64
66
161
196
196
231 AA;
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9 29
29
52
52
4 84
5 106
1 181
1 181
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FOR THE
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RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE; 96337999.

RA BULT C.J. WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

RA SUTTON G.G., BLAKE J.A., FITGGERALD L.M., CLAYTON R.A., GCCAYNE J.D.,

RA KERLAVAGE A.R., DOUGHERRY B.A., TOMB J.F., ADAMS M.D., REICH C.I.,

RA OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

RA SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

RA COTTON M.D., ROBERTS K.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

RA COTTON M.D., ROBERTS K.M., HURST M.A., KAIKE B.F., BORDDVSKY M.,

RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

SCIENCE 273:1058-1073(1006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y503_METJA Length: 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P81311;
15-JUI-1998 (Rel. 36, Created)
15-JUI-1998 (Rel. 36, Last sequence update)
15-JUI-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL PROTEIN MJ0703.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschii.
Archaea; Euryarchaeota; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67500; AAB98494.1; -. TIGR; MJ0503; -.
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                                                                                                                        ence 273:1058-1073(1996).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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06 AA; 45364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Y788\_BORBU

Length: 440

151 101

NRNIIRPLLE

VSRLEIENFL KENGANYIAL EHVKGFCDLY

SLNNIGEFVD AHNENDQIET NIALQIKKCD

STNAQNLYLR IIMRFFQGSE

YSFDLKTFLD FPKYLVFRLI FKILNSEGIA AKVSYKALNE AFKVEINRKI

5,1

RSDNEQNQEI

MHFLDENIQI KIDKFYKKNS

LDKNRVIVAF

SGGADSTALL LNLKYYLSNN

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Y70A_METJA Length: 102
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TRANSMEM
TRANSMEM
TRANSMEM
                              EMBL; AE00117
TIGR; BB0788;
Hypothetical
SEQUENCE 44
                                                                                                                                                                                                                                                                     MEDLINE; 98065943.

MEDLINE; 98065943.

FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A., MAITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M. DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D., HANSON M., PATERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M., VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J., UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C., GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B., SMITH H.O., VENTER J.C.;

"Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorfert"
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         burgdorferi.";
Nature 390:580-586(1997).
-i- SIMILARITY: BELONGS TO THE UPF0072 (MESJ/YCF62) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 35210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
HXPOTHETICAL PROTEIN BB0788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y788_BORBU
051728;
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                                                              AE001177; AAC67121.1; -. BB0788; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U67517; AAB98706.1; MJ0703.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          email to license@isb-sib.ch).
                              al protein.
440 AA; 51471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Transmembrane.

14 34 POTENTIAL.

35 55 POTENTIAL.

76 96 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  / B31;
February 14,
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2336A893 CRC32;
                                DF4B6E4A CRC32;
   2000
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                                                                                                                                                                                                                                                                                                                                                                                      GWINN M.,
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301

NNVLLKINDE

FLEKRHNKIN LIFKRDEKFY KPFDFILEVG

KWHSLSLGKI

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ROCCEPTTC
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HYPOTHETICAL 30.9 KD PROTEIN RV0953C.
RV0953C OR MYC10D7.21.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteria; Actinobacteria; Corynebacterineae; Mycobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SOCAYNE J.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAXTON R.A., GOCAYNE J.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAXTON R.A., GOCAYNE G.I., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOCHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., GUTTERBACK T.R., KELLEY J.M., PETTERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C., "COMPONIES GENOME SEQUENCE Of the methanogenic archaeon, Methanococcus Science 273:1058-1073(1996).
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2661 / ATCC
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Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
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POTHETICAL PROTEIN MJ0795.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
SIMILARITY: TO MJ1249.1, MJ0210.1 AND MJ0785.1.
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26 POTENTIAL.
51 POTENTIAL.
111 POTENTIAL.
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                  n; Actinobacteridae; Mycobacteriaceae; N
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IIAA_SEQUENCE 1.0
ID T988_METJA
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X MEDLINE; 98295987.

X MEDLINE; 98295987.

X ACOLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D. RA GONDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., RA GONDON S.V., EIGLMEIER K., BROWN D., CHILLINGWORTH T., CONNOR R., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., RA DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., RA HORNESY T., JAGELS K., KROCH A., MCLEAN J., MOULE S., MURPHY L., RAJANIREAM M.A., ROGERS J., RA TOLIVER S., OSBORNE J., OUALL M.A., RAJANIREAM M.A., ROGERS J., RA RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULISTON J.E. RA TAYLOR K., WHITEHEAD S., BARRELL B.G.; THE DECIPIER B. B.G.; THE DECIPIER B. BARRELL B.G.; THE DECIPIER B. BARRELL B.G.; THE COMPLETE GENOME SEQUENCE.";

RI "Decipiering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";

RI Nature 393:537-544(1998).

CC -1- SIMILARITY: TO M.TUBERCULOSIS RV2161C AND RV3079C.

CC -1- SIMILARITY: TO M.TUBERCULOSIS RV2161C AND RV3079C.
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                                                                                                                                                                  SEQUENCE FROM N.A.

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SETAIN-JAL-1 / DSM 2661 / ATCC 43067:

SX MEDLINE; 96337999.

REDLINE; 96337999.

REDLINE; 96337999.

RELAVE, 96337999.

RELAVE, 96337999.

RELAVE, 9637999.

RELAVE, 9637
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15-JUL-1998 (Rel. 36, Last sequence update)
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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AC P39220; P75632
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P39220; P75632;
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01-NOV-1997 (Rel.
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MEDLINE; 90108714.
KATO J., CHU L., KITANO K., DEVAULT J.D., KIMBARA K.,
CHAKRABARTY A.M., MISRA T.K.;
CHAKRABARTY A.M., MISRA T.K.;
synthesis in Pseudomonas aeruginosa: characterization of the algr2
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
11991 (Rel. 18, Dast annotation update)
12907HETICAL 13.0 KD PROTEIN IN ALGR3 3'REGION.
Pseudomonas aeruginosa.
Pseudomonas aeruginosa.
Pseudomonas proteobacteria; gamma subdivision; Pseudomonas group;
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or send a
                                                                                                                                                                                                                                                                                                                                                                                EMBL, M30145; -, NOT_ANNOTATED_CDS
PIR; J00150; J00150.
Hypothetical protein.
SEQUENCE 122 AA; 12967 MW; FEF
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                                                                        SEQUENCE FROM N.A.
BURKE D.H., ALBERTI M., ARMSTRONG G.A., HEARST J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
01-MAY-1992 (Rel. 22, Last annotation update)
11-MAY-1992 (Rel. 22, Created)
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MEDILINE; 97426617

BLATTNEER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.

RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,

GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,

MAU B., SHAO Y.;

"The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).
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EMBL; AE000116; AAC73167.1; -
ECOGENE; EG12610; Yabp.
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WEDLINE; 92334977.

YURA T., WORI H., NAGAI H., NAGATA T., ISH
YURA T., MIZOBUCHI K., NAKATA A.;

"SYSTEMBATLC SEQUENCING OF the Escherichia
the 0-2.4 min region.";

the 0-2.4 min region.";

Nucleic Acids Res. 20:3305-3308(1992).
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RUDD K.E.;

Unpublished observations (NOV-1994).
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                                                                                                                                                                                                                                                                           Rhodobacter.
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EMBL; Z11165; CAA77528.1; -. PIR; S17812; S17812.

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I I AA_SEQUENCE 1.0

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AC 031458;

DT 15-JUL-1998 (F
DE HYDOTHETICAL
CO Bactilus Staph
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                                                                                                                                                                                                                                                                                YBFT_BACSU
                                                                                                                                                                                                                                                                                                                          EMBL; AB006424; BAA33133.1; -.
EMBL; 299105; CAB12030.1; -.
HSSP; P09375; HOT.
SUBTILIST: BG12746; YBFT.
PROSITE: PS01161; GIC_GALMAC_ISOMERASE; 1
PFAM; PF01182; Glucosamine_iso; 1.
Hypothetical protein; Isomerase.
ACT_SITE
ACT_SITE
SEQUENCE 249 AA; 27289 MW; 20883DBC C
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15-JUL-1998 (Rel. 3
15-DEC-1998 (Rel. 3
HYPOTHETICAL 27.3 K
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                                                                                                             101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAGA K., LIU H., YASUMOTO K., TAKAHASHI H., YOSHIKAWA H.;
"Sequence analysis of the 70kb region between 17 and 23 degree of the
Bacillus subtilis chromosome.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group.
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
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201
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STRAIN-168;
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                                                                                                         AACKVYEDLI
MAEGPVTTDV PASILQKHNH VTVIADYKAA QKLKSASFS
                                                                                                                                                                   VTTFNLDEYA
                                                                                                                                                                                                                          ELCKLSAAII KEQIQAKKDA
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36, Last sequence update)
37, Last annotation update)
KD PROTEIN IN GLTP-CWLJ INTERGENIC
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                                                                                                         RQAGGIDVQI LGIGANGHIG
                                                                                                                                                                   GLSPSHPQSY
                                                      GDPVLVPRLA
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                                                                                                                                                                                                                      VLGLATGSTP VGLYKQLISD
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                                                      ISMGIKTIME
                                                                                                                                                                                                                                                                                                                                       CRC32;
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ID YC21_METJA
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[1]
SEQUENCE FROM N.A.
STRAIN-JAL-1 / DBM 2661 / ATCC 43067;
MEDLINE; 96337999. OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., FLAYTON R.A., GCLOEN A.
SUTTON G.G., BLAKE J.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
KERLAYAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., GLODEK A.,
OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
COUTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOM P.W., HANNA M.C.,
TOMMON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YC08_KLEPN
Q48454;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                  Q58618;
01-NOV-1997
01-NOV-1997
01-NOV-1997
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PFAM; PF00534; Glycos_transf_1; 1.
Hypothetical protein.
SEQUENCE 373 AA; 42641 MW; 4150
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 42.6 KD PROTEIN IN CPS REGION (ORF8).
Klebsiella pneumoniae.
Riebsiella proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                               351
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J. Bacteriol. 177:1788-1796(1995).
                                                                                                                                                                                                                                  Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                 HYPOTHETICAL
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MEDLINE; 95204345,
ARAKAWA Y., WACHAROTAYANKUN R., NAGATSUKA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation updat
L PROTEIN MJ1221.
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s synthesis
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KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus

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SO STITE
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STRAIN-AVONDORT;
REITH M.E., MUNHOLLAND J
"Complete nucleotide seq
genome.";
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphyra purpurea. Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT 1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 32.4 KD PROTEIN YCF38 (ORF291)
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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EMBL; U38804; AACO8207.1; -.
MENDEL; 10386; PORpu.ycf38;
Chloroplast; Hypothetical processes and the second second
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                                                                                                                                                                                                                                                                                    nt Mol. Biol. Rep. 13:333-335(1995).
SIMILARITY: BELONGS TO THE YCF38 FAMILY.
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128 148 POTENTIAL.
177 197 POTENTIAL.
210 230 POTENTIAL.
236 POTENTIAL.
236 POTENTIAL.
261 281 POTENTIAL.
299 AA; 32538 MW; 8E4A08F7 CRC32;
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     etical protein.
32427 MW; 921437DB CRC32;
                                                                                                                                                                                                                                                                                                                                                   sequence of the Porphyra
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ټ.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bangiophyceae; Bangiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORF291).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bangiaceae;
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182 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
STRAIN=KIZ / MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last and
15-JUL-1998 (Rel. 36, Last and
HYPOTHETICAL FIMBRIAL-LIKE PRO
EMBL; AE000196; AAC74024.1; -.
ECOGENE; EC13709; YCEQ.
PFAM; PF00419; Fimbrial; 1.
Hypothetical protein; Fimbria;
Hypothetical protein; Pimbria;
SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-i- SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
Bacteria; Proteobacteria;
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annotation updat
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IN PEPN-PYRD INTERGENIC REGION
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OSGEDDDAG
Escherichia coli.
Bacteria; Proteobacteria;
                         YCGZ.
                            P75991;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 8.8 KD PROTBIN IN ICDC-MINE INTERGENIC
                                                                                             STANDARD;
  gamma
                                                                                              PRT;
  subdivision;
                                                                                              78
                                                                                              8
  Enterobacteriaceae;
                                     REGION
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FANQASSDAA THVALQMYMN DGTTAITPDT

DVSATKLQTN AFITVVCATS

GQVSGVQIDV PIELKDCDTT

VTKNATETEN

SVMAADDNAI

TDGSVTFNGK

182 F 19025 MW;

a; Signal.

POPORTIAL.

HYPOTHETIAL FIMBRIAL-LIKE PROTEIN YCBQ

; CE190E78 CRC32;

February 14, 2000 08:03 Type: P Check:

YC38\_PORPU

Length:

291

February 14,

2000 08:03 Type:

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Check: 4681

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YCGZ_ECOLI Length: 78
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01-0CT-1996 (Rel. 34
01-NOV-1997 (Rel. 35
01-NOV-1997 (Rel. 3
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MEDLINE; 97426617.

BLATTINER F.R., PLUNKETT G. III, BLOCH C.A.,

RILEY M., COLLADO-VIDES J., GLASNER F.D., R

GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GO
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                                                                                                                                               AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., AIRA H., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H. KREMOTO K., KIMA K., KIMURA S., KITAKAWA M., KITAKAWA M., WAKINO K. MASHLMOTO K., KIM S., KIMURA S., KITAKAWA M., MOTOMURA K., NAKAMURA Y., MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y., MASHLMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAKEMOTO K., WADA C., YAMANOTO Y., YANO M., SUDMILTED (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       STRAIN-K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT
RILEY M., COLLADO-VIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 1.0
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STRAIN-K12 / 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Bacteria; Proteok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000215; AAC74248.1; -. ECOGENE; EG14288; YCgZ.
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[1]
                                                                                MEDLINE, 90
CHA M.-K.,
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      Science
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STRAIN-K12 / MG165
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                                                                  Thioredoxin-linked 'thiol peroxidase'
                                                                                                                        EQUENCE
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                                       Biol. Chem.
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nce 277:1453-1474(1997).
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                                                                                                                        OF 221-262
                                                       la coli
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                                          270:28635-28641(1995)
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35,
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                                                                                                                        FROM
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, Last sequence update)
, Last annotation update)
PROTEIN IN TPX-FNR ITERG
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                                                                                                                        N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma
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                                                                     from
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                                                                    periplasmic
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YCJI_ECOLI Length: 262
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STANDARD;

YCIZ_ECOLI

977333; P76841;

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annoctation update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
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This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                   AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H. KASHIMOTO K., KINAKAWA M., KITAKAWA M., KITAKAWA M., MAKINO K. MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.; SUDMILTED (DEC-1996) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., P
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A.,
MAU B., SHAO Y.;
MAU B., SHAO Y.;
Science 277:1453-1474(1997).
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EMBL; D90771; CAB20835.1; -.
EMBL; D90770; CAB20825.1; -.
EMBL; U33213; -; NOT_ANNOTATED_CDS.
ECOGENE; EG13906; ycji.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished observations (MAR-1996).
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                                                                                                                                                            REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                    coli K-12.";
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                                                                              restrictions
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YCQ5_YEAST Length: 317 February 14, 2000 08:03 Type: P Check:
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 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 36.3 KD PROTEIN IN POL4-SRD1 INTERGENIC REGION
YCR015C OR YCR15C.
                                                                                                                                                                                                                                                                                                  EMBL; X59720; CAA42332.1; -. PIR; S19425; S19425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
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EMBL; D90770; CAB20810.1; -.
EMBL; D90771; CAB20837.1; -.
EMBL; D90772; CAB20853.1; -.
EMBL; D90772; CAB20853.1; -.
ECOGENE; EG13923; YCJZ.
PROSSITE; PS00044; HTH_LISR_FAMILY; 1.
PFAM; PF00126; HTH_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Transcription regulation; DNA-binding. DNA_BIND 21 41 H-T-H MOTIF (POTENTIAL). SEQUENCE 299 AA; 33481 MW; 4B9337F1 CRC32;
                                                                                                                                                                 51
                                                                                                                                                                                                                                                             ypothetical protein.
EQUENCE 317 AA; 36264 MW; 0426F1E5 CRC32;
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VKSWDSLKDL
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                                INPQENPSKF
                                                                                                SINWSKEFIH
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                                                                 SDKVKILGEI
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IMQVTKM
                                                               LDKIDSGCNK
                                                                                              EVIGDRRLKN
                                                                                                                                LDQMKTFARD
                                                                                                                                                                 LLSSGVPTII
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                              IKITEKIIGI
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                              PKDKISSFEA DNGPAWLQFC EKEGGKGAYI
                                                               EGNSCSYWYI GDSETDLLSI LHPSTNGVLL
                                                                                                SHIFCNDLKK
                                                                                                                                QNHDDCLLRD
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                                                                                              GEFDCRLLTG
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ID YDM1\_SCHPO

STANDARD;

PRT;

131

B

YDSA\_SCHPO

Length: 174

February 14,

2000

08:03

Type: P

Check:

8869

MTSQLEKEAR EWIEETLHTK LNAQLDLLDQ LQSGVILCRI CKEALGANIR

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YDM1_SCHPO
                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIRS 972;
GENTLES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.,
GENTLES S., CHURCHER C.M. BARRELL B.G., RAJANDREAM M.A.,
SUBMILTES (AUG-1997) to the EMBL/GenBank/DDBJ databases.
SUBMILTER (AUG-1997) TO YEAST YOR367W AND TO CALPONINS.
 Hypothetical
SEQUENCE 1
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SKELTON J., CHURCHER C.M., WOOD V., BARRELL B.G., RAJAND SUBMITTED (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: TO M.JANNASCHII MJ0531.
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15-JUL-1998
15-JUL-1998
15-JUL-1998
                                 EMBL; 298530; CAB11057.1; -.
                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
HYPOJHETICAL 20.1 KD PROTEIN C4F8.10C IN CH
SPAC4F8.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z95396; CAB08759.1; -.
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11 protein.
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(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
(Rel. 36, Last annotation update)
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20141 MW;
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2DB8876B CRC32;
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IN CHROMOSOME I.
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                                                                                                                                                                                                                                      WOOD V.;
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YKESNMPFVQ MENISAFINY AQQVVHVPSQ DMFQTSDLFE RRNDEQVLRS

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ID YER4_YEAST
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01-FEB-1995 ()
15-JUL-1998 ()
HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENTLES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
STRAIN-S288C / AB972;

DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO DIETRICH F.S., MULLIGAN J.T., CARPENTER J., CHEN E., CHERRY CHUNG E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., LEW H., LIN D., HYMAN R., KAYSER A., KOMP C., LASHRARI D., LEW H., LIN D., MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH TAYLOR P., WEI Y., KELTON M., BOTSTEIN D., DAVIS R.W.;
                                                                                                                                                                                                                                                                                                                                                                      301
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SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
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                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                   Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA;
                                                                                                                                                                                                                                  (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 36, Last annotation update)
L 14.3 KD PROTEIN IN PTP3-ILV1 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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36, Last sequence up
36, Last annotation
KD PROTEIN C6B12.16
                                                                                                                                                                   Saccharomyces.
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IN CHROMOSOME
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                                                                               ARAUJO
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YER4_YEAST
!!AA_SEQUENCE 1.0
ID YG29_BPSP1
AC P31653;
                                                                                                                             YF58_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YF58_MYCTU STANDARD; PRT; 1
Q10772;
01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
HYPOTHETICAL 16.4 KD PROTEIN RV1558.
RV1558 OR MTCY48.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                     Hypothetical
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U18839; AAB64639.1; -.
                                                 101 YDAREVFGDE
                                                                                                                                                                             EMBL; Z74020; CAA98333.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctinomycetales; Corynebacterineae; Mycobacteriaceae;
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                                                                          LRKTPLMRVE
                                                                                                                          Length: 148
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                                                                          HDGQYAIVAS
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                                                                                                                           February 14, 2000 08:03
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                                                                                                                                                      16347 MW;
                                                 VWPDYASYQT
                                                                          LGGAPKNPVW YHNVVKNPRV
                                                                                                    TYMKSGGTEG
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                                                                                                                                                      7F320812 CRC32;
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                                                                                                    TQLQGKPVIL
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    YGK9_YEAST
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01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
HYPOTHETICAL 16.2 K
Bacteriophage SP01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEAST P53138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGK9_YEAS
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                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 97197974.
PAOLUZI S., MINENKOVA O., CASTAGNOLI L.;
"The genes encoding the transcription factor yTAFII60, the G4p1
protein and a putative glucose transporter are contained in a 12.3 kb
DNA fragment on the left arm of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 12.4 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION
YGL109W OR G3065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X60728; CAA43135.1; -.
PJR; S21504; S21504.
Hypothetical protein.
SEQUENCE 148 AA; 16183 MW;
                                                                                                                                                            EMBL; X97644; CAA66243.1; -. EMBL; Z72631; CAA96815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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Length: 107
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                                                                                       107 AA; 1
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    February
                                                                                  12435 MW;
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, Last sequence update)
, Last annotation update)
, Last annotation update)
PROTEIN IN GENE 29 5'REGION.
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    14, 2000
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                                                                                  349DFDE6 CRC32;
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    08:03
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Type: P
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    Check:
    6897
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!!AA_SEQUENCE 1.0
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01-FEB-1995;
01-FEB-1995;
01-NOV-1995;
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MEDLINE; 93345814.
WRAY L.V. JR., FISHER S.H.;
"The Streptomyces coelicolor glnR gene encodes a protein similar other bacterial response regulators.";
Gene 130:145-150(1993).
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
01-NOV-1995 (Rel. 32, Last annotation
HYPOTHETICAL PROTEIN IN GLNR 3'REGION
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 TLRPPLG
                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Stre
                                               EMBL; L03213; AAA02839.1; -.
PIR; PN0644; PN0644.
HSSP; P15039; 1PRV.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                        ria; Actinobacteridae;
Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                         e update)
ion update)
ion (FRAGMENT).
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YGLR\_STRCO Length: 66 February 14, 2000 08:03 Type: P Check: 9954

Hypothetical protein NON\_TER 66 ( SEQUENCE 66 AA; 7(

66 7094 MW;

502F47A4 CRC32;

 $\vdash$ MAKVTRDDVA RLAGTSTAVV SYVINNGPRP VAPATRERVL AAIKELGYRP

51 DRVAQAMASR RTDLIG

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!!AA_SEQUENCE 1.0
                                 SEQUENCE FROM N.A.

STRAIN-EP713;
MEDLINE; 89251194.

MEDLINE; 89251194.

"Characterization of double-stranded RNA genetic elements associated "Characterization of double-stranded RNA genetic elements associated with biological control of chestnut blight; organization of terminal domains and identification of gene products.";

EMBO J. 8:657-663 (1989).

-I- MISCELLANEOUS: DOUBLE-STRANDED RNA GENETIC ELEMENTS ARE ASSOCIATED WITH BIOLOGICAL CONTROL OF THE FUNGAL DISEASE CHESTNUT BLIGHT.

THIS DS-RNA ARE ASSOCIATED WITH HYPOVIRULENCE. THEY ARE LOCALIZED IN THE CYTOPLASM.

-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C7.
                                                                                                                                                                                                                                                                                                                                                                    p10941;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
ELEMENT [CONTAINS: P29 PROTEINASE]
ELEMENT [CONTAINS: P29 PROTEINASE]

CONTAINS: P29 PROTEINASE]

CONTAINS: P29 PROTEINASE]
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Eukaryota; l
                                                                                                                                                                                                                                                                                                         Diaporthales;
                                                                                                                                                                                                                                                                                                                                                             Cryphonectria parasitica (Chesnut blight fungus) (Endothia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRYPA
                                                                                                                                                                                                                                                                                                         Fungi; Ascomycota;
es; Valsaceae; Cryp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                       cota; Euascomycetes; Pyrenomycetes; Cryphonectria.
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MAAQNPLADI QYYKRYKAKR RMEGQKKNSC TIAYIDSLQY YCRRSLSHKS

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YHA1_CRYPA Length: 319
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PIR; S03833; S
                                                                                                                                                                                                                                                                                                                                          EMBL; X96983; CAA65704.1; -.
EMBL; Z99108; CAB12749.1; -.
SUBTILIST, BG11598; XHCT.
PROSITE; PS01129; PS1_RLU; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@1sb-sib.ch).
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Bacteria; Firmicuttes; Bacillus/Clostridium group;
Bacillus/StaphyLococcus group; Bacillus.
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151
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NOBACK M.A., TERPSTRA P., HOLSAPPEL S., VENEMA G., B

"A 22 kb DNA sequence in the cspB-glpPFKD region at

Bacillus subtilis chromosome.";

Microbiology 142:3021-3026(1996).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPGPLSHGDL RRLRTPDGVC KCQVHFELPT VLKSGSTGTV
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                                                 IATHPNEDGQ
                                                                                                      SVLNNMIVKK GDRVFIDLQE
                                                                                                                                                           MNQKGRGLEI LINEKQDGQW
                                                                                                                                                                                                                                                                                                                    TE; PS01129;
PF00849; YA
                                                                                                                                                                                                          Length: 302
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                                                                                                                                                                                                                                                                                                                 29; PSI_RLU; 1.
YABO; 1.
                                                                                                                                                                                                                                                               Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YCYLSAIVDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QRTKELDSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHVYHVVDA
                                                 TGTLANLIAY
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                                                                                                                                                                                                             February 14,
                                                                                                                                                                                                                                                                     33740 MW;
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                                                 HYQINGETCK
                                                                                                      SEASSVIPEY
                                                                                                                                                           LFSVLKTALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                     2EB71306 CRC32;
                                                                                                                                                                                                                2000
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                                                 VRHVHRLDQD TSGAIVFAKH
                                                                                                         GELDILFEDN HMLIINKPAG
                                                                                                                                                           ASKPVIQDWM SHQQIKVNHE
                                                                                                                                                                                                             08:03 Type: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYQAILGLAE
   KKGTINPPIG
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t 75 degrees
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IP YHGN_ECOLI
AC P46851;
DT 01-NOV-1995 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HYPOTHETICAL 48.9 KD PROTEIN IN RPL14B-GPA1 II
YHR003C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHG3_YE
P38756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
DU Z., FAVELLO A., FULTON L., GATTING S., GEISEL C., KIRSTEN J.,
KUCABA I., HILLIER L., JIER M., JOHNSTON L., HAGSTON Y.,
LATRRILLE P., LOUIS E.J., MACRI C., MARDLIS E., MENEZES S., MOUSER L.,
NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
VAUTIN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288C / AB972;
MEDLINE; 94378003.
JOHNSTON M., ANDREWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome {\bf viii.}";
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                                                                                                    351
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                                                                                                                                                                                                                                                                                                                                                                          EMBL; U10555; AAB68430.1; --
PIR; S46801; S46801
PFAM; PF00899; ThiF_family; 1.
Hypothetical protein
SEQUENCE 429 AA; 48883 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 265:2077-2082(1994).
-1- SIMILARITY: STRONG, TO YEAST YKLO27W. SOME, COFACTOR BIOSYNTHESIS PROTEIN A (MOAA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAUDIN
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                                                                                                                                                                                             GVATKSDPTR
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                                                                         LDGEKLTAVY
                                                                                                      VEEMFRGKSP
                                                                                                                                                                DPRRDDILSP
                                                                                                                                                                                                                           KAWTKENSHD
                                                                                                                                                                                                                                                        IMI IDPENIS
                                                                                                                                                                                                                                                                                    HLFREQLARN YAFLGEEGMR KIKEQYIVIV GAGEVGSWVC
                                                                                                                                  VSGYPMKENE
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                               STANDARD;
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                                                                                                      ISGYSTKLAL
                                                                                                                                  VKNRLKFYDS
                                                                                                                                                                IDCEHRAINA
                                                                                                                                                                                             VSINDISMTE
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                                                                          SEEVLDFIER
                                                                                                                                                                                                                                                                                                                                              February 14, 2000 08:03 Type: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces.
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                                                                                                                                                                                                                           FIVDCLDNLE
                                                                          LFKEEEYYS
                                                                                                      TKWEANKEIS
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                                                                                                                                                                                                                                                                                                                                                                             709A28CF CRC32;
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                                                                                                                                                                                                                             SKYDLLEYAH
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                                                                                                                                                                                               KLRKRGIATG
                                                                                                        LTNVVLMTKE
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(Rel.

32, Created

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YHGN_ECOLI
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EMBL; AE
ECOGENE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
GOLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARR GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELLWELL T., GENTLES S., HAMLIN N., HOLGOY, DAVIES T., JACELS K., KROGH A., MCLEAN J., MUDLE S., MURPHY L., OLIVER S., OSBORNE J., QUALI M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEEGER K., SKELTON S., SQUARES R., SULSTON TAYLOR K., WHITEHEAD S., BARRELL B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  MEDLINE; 98295987.
COLE S.T., BROSCH
                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence
15-DEC-1999 (Rel. 39, Last annotatio
HYPOTHETICAL 18.1 KD PROTEIN RV1829,
RV1829 OR MTCY1ALL.14C.
                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                          STRAIN-H37RV;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                         Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
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TRANSMEM
TRANSMEM
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e complete genome sequence of Escherichia coli K-12.";
ence 277:1453-1474(1997)
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTE
SIMILARITY: BELONGS TO THE UPF0056 (MARC) FAMILY.
                                                                                                                                                                                                                                                                                  VILLQSSLFL
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                                                                                                                                                                                                                                                                                                                                                                          Length: 197
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4 2;

45 6

72 9

106 1;

139 1;

174 1

197 AA;
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(Rel.
L 21.5
                                                                                                                                                                                                                                                  STANDARD;
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37,
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                                                                                                                                                                                                                                                                                                                                                                                                 21490 MW;
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, Last annotation update)
PROTEIN IN ASD-GNTU INTERGENIC
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                               FLIAIKMIFP
                                                                                                                                                                                                                                                                                                                                                    TEPKRRRAIM
                                                                                                                                                                                                                                                                                                                                                                          08:03 Type:
                                                                                                                                                                                                                                                                                                                                                                                                 CRC32;
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                                                                                                                                                                                                                                                                                                                               SASGNSSGLP
                                                                                                                                                                                                                                                                                                                                                    VRELLIALLV
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                                                                                                                                          Mycobacterium
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                                                HOLROYD
                                                                                  HARRIS
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                                                                                  YJ96_MYCTU
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             PEGWAFEYSR FQEAQKREIV EHSYLVAQAH QIVEQAHKVA LEASSSGRAA
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YI29_MYCTU
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                                                                                                                                                                                                                                                                                                                                                   REPLINE; 9825987.

WEDLINE; 9825987.

AGENTAIN-H37RY;

COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.

GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F.,

BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,

ADAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S.,

ADAVIES R., DEFLIN K., FELTWELL T., GENTLES S., WIRPHY L.,

ADAVIES R., OSGELS K., KROGH A., MCLEAN J., MULE S., MURPHY L.,

AND LIVER S., OSBORNE J., OUAIL M.A., RAJANDREAM M.A., ROGERS J.,

AND LIVER S., SEBGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E.

RA RUTTER S., SEBGER K., SKELTON S., SOUARES S., SONARES R., SULSTON J.E.

RA TAYLOR K., WHITEHEAD S., BARRELL B.G.;

TOCOMPLETE GENOME SEQUENCE.";

RI "Deciphering the biology of Mycobacterium tuberculosis from the

RI COMPLETE GENOME SEQUENCE.";

RI Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1.0
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   EMBL; 274025; CAA98390.1; -. PFAM, PF00582; Usp; 2. Hypothetical protein. SEQUENCE 317 AA; 33879 MW
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RV1996 OR MTCY39.23C.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z78020; CAB01481.1; --
Hypothetical protein.
SEQUENCE 164 AA; 18114 MW
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation updat
HYPOTHETICAL 33.9 KD PROTEIN RV1996.
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رون معلم cal protein.
317 مم
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      MW;
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   AAFFB579 CRC32;
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Length: 317

February 14,

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IIAA_SEQUENCE 1.0
ID YJXX_ECOLI
AC P39411;
DT 01-FEB-1995 (F
DT 01-F
DT 01-FEB-1995 (F
DT 01-F
   OCCUPATO
                                                                                                                                                                                                         ID YJJX_ENTAE
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                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
01-FEB-1995 (Rel. 31, Last annotation update)
rypoTHETICAL PROTEIN IN TRPR 3'REGION (FRAC
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01-FEB-1995 (Rel. 31, Last sequence update)
01-ROV-1997 (Rel. 35, Last annotation update)
01-WFPOTHETICAL 18.6 KD PROTEIN IN TRPR-GPMB INTERGENIC REGION (F173).
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Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000509; AAC77347.1; -.
EMBL; J01715; -; NOT_ANNOTATED_CDS.
ECOGENE; EG12600; yjjX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U14003; AAA97290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA Sequence of the E. coll trpR gene and sequence of Trp repressor.";
Nucleic Acids Res. 8:1551-1560(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 95334362.
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Bacteria; Proteob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
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BURLAND V.D., PLUNKETT G.
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                                                                              update)
(FRAGMENT).
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IIAA_SEQUENCE 1.0
ID YXFF_ECOLI
AC P75677;
DT 15-JUL-1998 (
DT 15-JUL-1998 (
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OBERMALER B., PIRAVANDI E., RINKE M., DOMDEY H.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P46989;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 21.6 KD PROTEIN IN ATP12-RPL17B
YJL178C OR J0490.
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Nucleic Acids Res. 22:1821-1829(1994).
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MEDLINE; 94268903.
ARVIDSON D.N., ARVIDSON C.G., LAWSON C.L., MINER J., ADAMS
YOUDERIAN P.;
                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 249453; CAA89473.1; -.
Hypothetical protein; Transmembrane.
TRANSMEM 125 145 POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                   EGKKPAKKAG
   36, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   21605 MW;
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                                                                                                                                                                                                                   GTSWFTWLFL
                                                                                                                                                                                                                                                                        SHTWADKSIQ
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AEA06F63 CRC32;
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE; 92114051.

ODA K., YAMATO K., OHTA E., NAKAMURA Y., TAKEMURA M., NOZATO N.,

AKASHI K., KANEGAE T., OGURA Y., KOHCHI T., OHYAMA K.;

"Gene organization deduced from the complete sequence of liverwort

Marchantia polymorpha mitochondrial DNA. A primitive form of plant

mitochondrial genome.";

J. Mol. Biol. 223:1-7(1992).
PIR; S25969; S25969.
MENDEL; 2099; MARPO; Ymf27;1.
Mitochondrion; Hypothetical
SEQUENCE 69 AA; 7940 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Strep
Marchantiales; Marchantiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marchantia polymorpha (Liverwort) Mitochondrion.
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                                                                                                                        EMBL;
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STRALN-K12 / MG1655;
MEDLINE; 97428617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., RODE C.K., MAYLEW G.F.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYLEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     True complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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HYPOTHETICAL
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                                                                                                                  M68929; AAC09407.1; -.
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4 (Rel. 30, Last au
AL 7.9 KD PROTEIN:
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9 AA; 9014 MW;
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KD PROTEIN IN PROA-PERR INTERGENIC REGION
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Last sequence update)
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ROTEIN IN NAD6-NAD3 INTERGENIC
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ceae; Marchantia.
         Protein.
699EE385 CRC32;
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2000 08:03

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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., BURTON J., CONNELL.M., COPSEY T., COOPER J., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER

COULSON

SEQUENCE OF 53-170 FROM STRAIN-BRISTOL N2; MEDLINE; 94150718.

N.A. the

Submitted (FEB-1994) to

EMBL/GenBank/DDBJ

databases

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01-0CT-1996 (Rel. 301-0CT-1996 (Rel. 301-0C
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 19.1 KD PROTEIN PARZ.1 IN CHROMOSOME
K02Dl0.5 OR PARZ.1.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nemat
Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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P34496;
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DOMAIN
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MEDLINE; 96310631.
SEN-GUPTA M., LYCK R., FLEIG U., NIEDENTHAL R.K., HEGEMANN J.H.;
"The sequence of a 24,152 bp segment from the left arm of chromosome
XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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25 33
35 55
57 77
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KD PROTEIN IN PIK1-POL2 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n; Transmembrane.
33 POLY-SER.
55 POTENTIAL.
77 POTENTIAL.
15510 MW; 11A8B5FA CRC32;
                                                                                                                                                                                                                                                                               Nematoda; Secernentea; Rhabditia; Rhabditida;
Didea; Rhabditidae; Peloderinae; Caenorhabditis
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YNA1_CAEEL Length: 170 February 14, 2000 08:03
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PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWIKEEN
SIMS M., SWALIDON N., SMITH A., SONIHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WATESON A., WEINSTOCK L., WILKINSON-SPROAT J.,
WOLLDMAN P.,
"2.2 Mb of continuous professions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elegans.",
Nature 368:32-38(1994).
-!- SIMILARITY: TO PLASMID RK2 P116.
                                                                                                                                 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERT T., COOPER J.,
CRAXTON M., DEAR S., DU Z., DURSIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KRESHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WAISON A., WEINSTOCK L., WILKINSON-SPROAT J.,
WATERSON R., WAISON A., WEINSTOCK L., WILKINSON-SPROAT J.,
WOLLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1.0
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                                                                   elegans.";
Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                   WOHLDMAN
"2.2 Mb o
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EMBL; L14710; AAA28082.1; ALT_INIT
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WORMPEP; PAR2.1; CE
PFAM; PF00436; SSB;
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                                                                                                                                                                                                                                                                                                                    MEDLINE; 94150718.
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erans. **:
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170 AA; ]
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1 (Rel.
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28, Last sequence u.
29, Last annotation
KD PROTEIN R05D3.9
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IN CHROMOSOME
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February 14, 2000 08:03 Type: P Check:

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AKIDMTIPRK

RKGFTSQHEK GLEKFYEAVS

TAFMRHVNLQ

KETTEORAKE

EEAEDMWHIY SIDFDPGAQE DLERLNLALD

NLIRIGDIIK LHLKGRNIEE PAQAADVAAV

ASTIRKVVSE NDIVKLGAYH

51

DGTGFVVLMA VHTMLTVSVE

MKQFKRGIER

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YNC9_CAEEL
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NYPOTHETICAL 42.9 KD PROTEIN R74.6 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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                                                    EMBL; 236238; CAA85277.1; --
WORMED; R74.6; CE01059.
PFAM; PFOM605; RF1.1.
Hypothetical protein; Cell division; Meiosis; Mitosis
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Nuclear protein.
SEQUENCE 381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL
GARDINER A.;
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SEQUENCE FROM N.A.
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ical protein.
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      42878 MW;
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QVALRLADTK

AQGEVKALNQ FLELMSTEPD

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                                                                                                                                                                 STRAIN-ERISTOL N2;

MEDLINE; 94150718.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,

FULTON L., GARNNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,

JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,

LATREILLE P., LICHTNING J., LLOYD C., MORTINGE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWKEEN R.,

SIMS M., SMALDON N., SMITH A., SMITH M., SOUNHAMMER E., STADEN R.,

SULSTON J., THIERRY-MIEG J., THOMAS K., VADDIN M., VADGHAN K.,

SULSTON J., THIERRY-MIEG J., THOMAS K., VADDIN M., VADGHAN K.,

NAMALDON M. SMITH S., SMITH M., SOUNDERS D., STADEN R.,

SULSTON J., THIERRY-MIEG J., THOMAS K., VADDIN M., VADGHAN K.,

NAMALDON M. SMITH S., SMITH M., VADDIN M., VADGHAN K.,

NAMALDON M., SMITH S., SMITH M., VADDIN M., VADGHAN K.,

NAMALDON M., SMITH S., SMITH M., VADDIN M., VADGHAN K.,

NAMALDON M., SMITH S., SMITH M., SMITH M., VADDIN M., VADGHAN K.,

NAMALDON M., SMITH S., SMITH S., VADDIN M., VADGHAN K.,

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NAMALDON M., SMITH S., S
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
01-FEB-1996 (Rel. 33, Last annotation
HYPOTHETICAL 18.2 KD PROTEIN ZK632.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Phahditina: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                               WATERSON R., WATSON A., WOHLDMAN P.;
"2.2 Mb of contiguous nu
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
11-NOV-1990 (Rel. 16, Created)
11-NOV-1990 (Rel. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDWANN H.;
Submitted (MAR-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. NEUMANN H.;
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                                                                                                                                                     WEINSTOCK L., WILKINSON-SPROAT
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I!AA_SEQUENCE 1.0

ID YOXD_BACSU
AC P14802;

DT 01-DEC-1992 (F
DEC-1992 
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EMBL; 299114; CAB13743.1; -.
PIR; S01270; S01270.
HSSP; P1992; 2HSD.
SUBTILIST; BG11048; YOXD.
PROXITE; PS00061; ADH_SHORT; 1.
PEAM; PE00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a copyred the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or.send.an_email to license@isb-sib.ch).
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AHN K.S., WAKE R.G.;
"Variations and coding features of the sequence spanning the replication terminus of Bacillus subtilis 168 and W23 chromosomes."; cene 98:107-112(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P14802;
01-APR-1990 (Rel. 14, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN RTP-PELB INTERGENIC
(ORF238).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 88040469.
CARRIGAN C.M., HAARS
"Sequence features of subtilis chromosome.
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Bacteria; Firmicutes;
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STRAIN=168;
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Paa; 18180 MW;
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tent is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collaboration -
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YPDC_ECOLI
                              EMBL; DYNOUTH PROC.

ECOGENE; EG14450; YPDC.

ECOGENE; EG1441; HTH_ARAC_FAMILY_1; 1.

PROSITE; PS00124; HTH_ARAC_FAMILY_2; 1

PRAM; PF00165; HTH_2; 1.

PFAM; PF00165; HTH_2; 1.

Hypothetical protein; Transcription re
Hypothetical protein; Transcription re
DNA_BIND 200 219

DNA_BIND 205 AA; 32355 MW; 61FFAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P77396;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN DDG-GLK INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _SEQUENCE 1.0
YPDC_ECOLI
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 97436617.

BELATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V BLATINER F.R., PLUNKETT G. III, BLOCH C.A., RODE C.K., MAYHEW G.F., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Construction of a contiguous 874-kb sequence of the Escherichia of Kl2 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features."

DNA Res. 4:91-113(1997).

-!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 97349980.

YAMANOTO Y., AIBA H., BABA T., HAYASHI K., INADA T., ISONO K., YAMANOTO Y., AIBA H., BABA T., HAYASHI K., MIKI T., MITSUHASHI N., ITOH T., KURRA S., KITAGAWA M., MAKAMURA Y., NASHIMOTO H., MIZOBUCHI K., MORI H., NAKADE S., NAKAMURA Y., NASHIMOTO H., OSHLMA T., OYAMA S., SAITO N., SAMPEI G., SATOH Y., SIVASUNDARAM S., TAKAHASHI H., TAKAHASHI K., MASAMI H., TAKAHASHI H., TA
                                                                                                                                                                                                                                   EMBL; AE000326; AAC75441.1; -. EMBL; D90868; CAB22182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia.
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Length:
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238 AA;
   285
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25299 MW;
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February
                                                 Transcription regulation; DNA-binding
9 H-T-H MOTIF (BY SIMILARITY).
2355 MW; 61FFAA84 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLDPRIFIKT
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; 06381861 CRC32;
14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
2000 08:03
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Type:
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and
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!!AA\_SEQUENCE 1.0

DY PQQ\_KLEEN STANDARD; PRT; 271 AA.

AC P27509;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-AUG-1995 (Rel. 32, Last annotation update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE HYPOTHETICAL PROTEIN IN PQQA 5'REGION (ORF X)

101

PDHGNAAALV

EEAIFSAGIH

HKVSKVYYYM

201 151

EAREKLYGKE

AGVEYAEVSF

PNGC

INGFHQPDFV VFMPYKKDRH

IDISDTIEAK KOSLNAYKSO

FIPSKDSVST KYKDEKSLPA

RRCCOSETTION

Klebsiella pneumoniae. Bacteria; Proteobacteria;

gamma subdivision; Enterobacteriaceae;

(FRAGMENT)

SEQUENCE FROM N.A. Klebsiella.

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HARDER SOCIONARIA PROCESSO DE LA PRO
                                                                                                            YPJG_BACSU
                                                                                                                                                         EMBL; L38424; AAA92876.1; -.
EMBL; L47709; AAB38444.1; -.
EMBL; Z99115; CAB14.63.1; -.
SUBTILIST; BG11212; YPJG.
Hypothetical protein.
SEQUENCE 224 AA; 24806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P42981;
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a copyred three three swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and is entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of the Bacillus subtilis chromosome region the serA and kdg loci cloned in a yeast artificial chromosome. Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168 / MARBURG;
MEDLINE; 96349105.
SCROKIN A.V., AZEVEDO V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
STRAIN-168 / MARBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpJG OR JOJG.

Bacillus subtilis.

Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
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   SLRKEEAAEA
                                                      MYNADVLAFG
                                                                                                         Length: 224
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ARILGADKRI
                                                         AHSDDVEIGM GGTIAKFVKQ
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32, Last sequence update)
37, Last annotation update)
KD PROTEIN IN DAPB-PAPS INT
                                                                                                            February
                                                                                                                                                                  24806 MW;
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QLTLPDRGLI
                                                                                                            14,
                                                                                                                                                                      DF897440 CRC32;
                                                                                                            2000 08:03 Type: P Check:
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MSDQAIRSIV
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tent is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
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YPQQ_KLEPN Length: 271
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P77031; P76634; P76635;
01-NOV-1997 (Rel. 35, Class
01-NOV-1997 (Rel. 35, Lass
01-NOV-1997 (Rel. 35, Lass
01-NOV-1997 (Rel. 35, Lass
HYPOTHETICAL 46.8 KD PROTI
SEQUENCE FROM N.A.

STRAIN-K12;
AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
AIBA H., BABA T., ISONO K., ISONO S., ITOH T., KANAI K.,
IKEMOTO K., INADA T., ISONO K., KIMBAS S., KITAAWA M.,
KASHIMOTO K., KIM S., KIMBAS S., KITAAWA M.,
KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H.,
KOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T.,
SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C.,
YANAMOTO Y., YANO M.;
SUBDELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-MEDICINE; 974.26617.

MEDICINE; 974.26617.

MEDICINE; 974.26617.

MEDICINE; 974.26617.

MEDICINE; 974.26617.

MEDICINE; 974.26617.

MAYHEW G.F.

GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,

GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,

MANU B., SHAO Y.;

MENU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 1.0
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MO1. Gen. Genet. 232:284-294(1992).
-i- FUNCTION: NOT KNOWN.
-i- SIMILARITY: BELONGS TO PEPTIDAS:
-i- SIMILARITY: TO AN ORF IN THE 3'.
-i- A.CALCOACETICUS.
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MEDLINE; 92212293.
MEULENBERG J.J.M.,
                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEULENBERG J.J.M., SELLINK E., RIEGMAN N.H., POSTMA P. 
"Nucleotide sequence and structure of the Klebsiella programme."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                      The complete genome sequence of Escherichia Science 277:1453-1474(1997).
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PS00869; F
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35, Last sequence update)
35, Last annotation update)
KD PROTEIN IN CYSJ-ENO INTERGENIC
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RF IN THE 3'REGION OF PQQ-III
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                                                                                                                                                                                                                            coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae;
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I YOEK_ECOLI
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                                                             SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE 97426617.
BLATTNER F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
GREGOR J, DAVIS N.W., KI
MAU B., SHAO Y.;
                                                                                                                                                                                                     P77136;
01-NOV-1997
15-JUL-1998
15-JUL-1998
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TRANSMEM
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                                  Science
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EMBL; D90893; CAB22504.1; -
ECOGENE; EG13174; YQCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                401
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SEQUENCE OF 14-141 FROM N.A. STRAIN-K12 / MG1655; ROBERTS D., ALLEN E., ARAUJO
                                                                                                                                                                                            HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                       The
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                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence complete genome sequence 277:1453-1474(1997).
                                                                                                                                                                                                                                                                               VIVETELLEQ KIRTADSAPA MASSK
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                                                                                                                                                                                                                                                                                                                                                                                       LAVETMWVFS RFAPDDSTSL KTVIIIYSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                 MSTFGIAAII LYAPSGVIAD KFSHRKMITS AMIITGLLGL LMATYPPLWV
                                                                                                                                                                                                                                                                                                                                              YGMSLVAASY MGIVINKIFR
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                                                                                                                                                                                           (Rel. 35, Created)
(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
L 16.3 KD PROTEIN IN KDUI-LYSS INTERGENIC
                                                                                                                                                                                                                                                STANDARD;
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                                                                          T G. III, BLOCH C.I
S J., GLASNER F.D.
KIRKPATRICK H.A.,
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                                                                                                                                                               subdivision;
                                                     Escherichia coli K-12.";
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                                                                        C.A., PERNA N.T., BURLAND V.D., RODE C.K., MAYHEW G.F., A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                     LPAAEAYRNM WLMGMAALGM
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CHUNG

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I!AA_SEQUENCE 1.0 ID YRBC_HAEIN AC P45028;
                                                                                                                                                                                                      YR7B_ECOLI Length: 169
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                                                                  151 AMASAVDTVT
                                                                                                                                                                                                                                    EMBL; M55249; AAA23393.1; -.
PIR; JQ0857; JQ0857.
Transposable element; Hypothetical protein.
SEQUENCE 169 AA; 18129 MW; 9D36865A CRC32;
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Retron for the 67-base multicopy single-stranded DNA from Escherichia coli: a potential transposable element encoding reverse transcriptase and Dam methylase functions ", proc. Natl. Acad. Sci. U.S.A. 87:9454-9458(1990).
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01-WAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
HYPOTHETICAL 18.1 KD PROTEIN (ORFB) (RETRON EC67).
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000369; AAC75888.1; ALT_INIT.
EMBL; U83187; AAB40288.1; -.
ECOGENE; EG13274; YGEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUNCAN M., FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C.,
LEW H., LIN D., NAMATH A., OEFNER P., SCHRAMM S., DAVIS
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia.
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P21316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AA;
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              STANDARD
                                                                GLGASFGLL
                                                                                                                                   DLTEDSTLVD GFLAQIHCLP CVPINEVAKE KLPHYVMSAT
                                                                                                                                                                     HFDEACRAFA LRHNLVQLAE RAGMNVQILR
                                                                                                   VSGDVKTSAG
                                                                                                                                                                                                    February 14, 2000 08:03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INOUYE S.;
                                                                                                   RRDAISSINS
              PRT;
              214
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R.W.;
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IIAA_SEQUENCE 1.0
ID YRKG_BACSU
AC P54434;
DT 01-0CT-1996 (F
DT 01-0CT-1996 (F
DT 01-0CT-1996 (F
DE HYPOTHETICAL 4
GN YRKG.
OS BACILLUS SUBTI
OC BACILLUS FILTI
OC BACILLUS FILT
OC BACILLUS FILTI
OC BACILLUS FIL
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Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus.
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#EDIINE: 9530630.

#EDIINE: 9530630.

#EDIINE: 9530630.

#ERISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

#ERISCHMANN R.D., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,

#ERICANAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,

#ECKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GCCAYNE J.D.,

#ECKENNEY K., SUTTON G., FILL L.I., GLODEK A., KELLEY J.M.,

#EIDMAN J.F., PHILLIPS C.A., SPRIGGS T, HEDBLOM E., COTTON M.D.,

#INE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,

#EINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,

#EINE L.D., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                            STRAIN-168 / JH642;
KOBAYASHI Y., MIZUNO M.,
SATO T., TAKEUCHI M.;
Submitted (MAY-1996) to t
                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
HYPOTHETICAL 4.2 KD PROTEIN IN BLTR-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL PROTEIN HI1084 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
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Bacteria; Proteobacteria;
              This SWISS-PROT entry is copyright.
between the Swiss Institute of Bio
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TIGR; HI1084; -.
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-!- SIMILARITY: STRONG, TO E.COLI YRBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VENTER J.C.
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18-DEC-1999 (Rel. 38, Last sequence update)
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GOLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRI: GOLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRI: GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVLES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., DLIVER S., OSBORNE J., QUALL M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON TAYLOR K., WHITEHEAD S., BARRELL B.G.;
TDECIPHETING the blology of Mycobacterium tuberculosis from the complete genome sequence. ", whitehead s., barrell b.G.;
Nature 393:537-544(1998).

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                               SEQUENCE 1.0
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Bacillus subtilis.

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                                                                                                                            F5966.8.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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F59C6.8.
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EMBL; Z99123; CAB15797.1; -.
PIR; S39739; S39739.
SUBTILIST; EG10630; YWFF.
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MEDLINE: 95020537.

GLASER P., KUNST F., ARNAUD M., COUDART M.P., GONZALES W.,
HULLO M.F., IONESCU M., LUBOCHINSKY B., MARCELINO L., MOSZER I.
PRESECAN E., SANTANA M., SCHNEIDER E., SCHWEIZER J., VERTES A.,
RAPOPORT G., DANCHIN A.;
"Baccillus subtilis genome project: cloning and sequencing of the
"Baccillus subtilis genome project: cloning and sequencing of the
Mol. Microbiol. 10:371-384(1993).

MOL. Microbiol. 10:371-384(1993).

MOL. MICROBIOL. 10:371-384(1993).
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WILKINSON J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO A FAMILY OF C.ELEGANS PROTEINS THAT GROUPS
C27A7\_2, C33H5.2, C35A5.5, F13G3.3, F59C6.8, F49C12.5, R07B7.12

AND ZK381.2

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EMBL; L14063; AAA18532.1; MAIZEDB; 63528; -. PFAM; PF00891; Methyltrans
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. NKH31; TISSUE-ROOT;
STRAIN-CV. NKH31; TISSUE-ROOT;
MEDLINE; 94105316.
JOHN I., WURTELE E.S., COLBERT J.T.;
HELD B.M., WANG H., JOHN I., WURTELE E.S., COLBERT J.T.;
HELD B.M., WANG H., JOHN I., WURTELE E.S., COLBERT J.T.;
PART METALLY COMING for an O-methyltransferase accumulates preferentially in maize roots and is located predominantly in the region of the endodermis.";
Plant Physiol. 102:1001-1008(1993).

-I. FUNCTION: MAY BE INVOLVED IN THE O-METHYLATION OF SUBERIN
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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Ol-FEB-1996 (Rel. 33, Last sequence update)
Ol-CCT-1996 (Rel. 34, Last annotation update)
O-ESTHYLTRANSFERASE ZRP4 (EC 2.1.1.-) (OMT).
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SIMILARITY: TO OTHER OMTS REQUIRING S-ADENOSYL-L-METHIONINE AS
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                                                                                                                                                                                                                                                                                                            PHENYLPROPANOID PRECURSORS
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Methyltransf_2; 1.
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ZRP4\_MAIZE Length: 364 SQ 151 101 Transferase; Methyltransferase. SEQUENCE 364 AA; 39583 MW; 51 CIFKHTHGRG DMFESIPPAD ISSLVDVGGG YTLTPVSRLL AASLSQILSK VHLHPSRVSS LRRLMRVLTT INVFGTQPLG MELSPNNSTD AVLLKSVLHD WDHDDCVKIL KNCKKAIPPR EAGGKVIIIN QSLLDAQLEL WHTTFAFMKS MALKSAIHLR IADAIHLHGG IGAAAQAISK AFPHVKCSVL IWELTKODAT FDALVNDGLA SDSQLIVDVA IKQSAEVFQG IGSOSSQLAQ TPLAAMVLDP February 14, 2000 08:03 Type: P 3067DB07 CRC32; DLAHVVAKAP TIVSPFSELG THIDVQFIAG AWFQHELPDP GGSDDDSEPV Check:

MVVGAGPSDM

KHKEMQAIFD VYIMFINGME

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IPVLGVRSII EVYF

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